GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 16.5871 Seconds
(without alignments)
3219.466 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	931	100.0	893	3	AAY95012	Aay95012 Human sec
2	931	100.0	983	6	ABU11573	Abu11573 Human MDD
3	931	100.0	1178	3	AAY71311	Aay71311 Human neu
4	931	100.0	1192	3	AAY56967	Aay56967 Human MAG
5	931	100.0	1192	4	AAB82349	Aab82349 Human NOG
6	931	100.0	1192	4	AAU04591	Aau04591 Human Nog
7	931	100.0	1192	5	ABG30938	Abg30938 Human Nog
8	931	100.0	1192	5	ABP68600	Abp68600 Human pan
9	931	100.0	1192	5	ABB81078	Abb81078 Human neu

10	931	100.0	1192	6	ABR59667	Abr59667 Human Nog
11	928	99.7	200	4	AAB64514	Aab64514 Human sec
12	927	99.6	199	2	AAW53947	Aaw53947 Human NSP
13	927	99.6	199	2	AAW78313	Aaw78313 Fragment
14	927	99.6	199	3	AAB12805	Aab12805 Human NSP
15	927	99.6	199	4	AAB82348	Aab82348 Human NOG
16	927	99.6	199	5	ABB81080	Abb81080 Human neu
17	927	99.6	373	3	AAY53624	Aay53624 A bone ma
18	927	99.6	373	3	AAY56969	Aay56969 Human MAG
19	927	99.6	373	3	AAB24242	Aab24242 Human Nog
20	927	99.6	373	4	AAB82350	Aab82350 Human NOG
21	927	99.6	373	5	AAM47954	Aam47954 Human RTN
22	927	99.6	373	5	ABG30937	Abg30937 Human Nog
23	927	99.6	373	5	ABP68601	Abp68601 Human pan
24	927	99.6	373	5	ABB81079	Abb81079 Human neu
25	923	99.1	291	4	AAM93484	Aam93484 Human pol
26	918	98.6	199	2	AAY35903	Aay35903 Extended
27	908	97.5	361	3	AAY71385	Aay71385 Alternati
28	908	97.5	1163	3	AAY71310	Aay71310 Rat neuri
29	908	97.5	1163	3	AAY71384	Aay71384 Alternati
30	908	97.5	1163	5	ABB81074	Abb81074 Rat neuro
31	906	97.3	199	3	AAY71559	Aay71559 Rat Nogo
32	906	97.3	359	3	AAY71558	Aay71558 Rat Nogo
33	906	97.3	403	3	AAY71563	Aay71563 Rat Nogo
34	906	97.3	1162	3	AAY71557	Aay71557 Rat Nogo
35	905	97.2	379	7	ADB85283	Adb85283 Rat fooce
36	904	97.1	199	5	ABB81077	Abb81077 Rat neuro
37	904	97.1	360	3	AAY71383	Aay71383 Rat neuri
38	904	97.1	360	5	ABB81076	Abb81076 Rat neuro
39	904	97.1	522	3	AAY71312	Aay71312 Rat neuri
40	894.5	96.1	642	2	AAW58383	Aaw58383 Human sec
41	894.5	96.1	642	4	AAB90682	Aab90682 Human BG1
42	886	95.2	199	5	ABG30939	Abg30939 Human Nog
43	851	91.4	175	2	AAW78194	Aaw78194 Human sec
44	682	73.3	202	4	AAB64513	Aab64513 Gene 27 h
45	682	73.3	208	3	AAB12808	Aab12808 NSPC prot

ALIGNMENTS

```
RESULT 1
AAY95012
ID   AAY95012 standard; protein; 893 AA.
XX
AC   AAY95012;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human secreted protein vb22_1, SEQ ID NO:64.
XX
KW   Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW   blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW   infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW   neurodegenerative disease; asthma; contraceptive.
XX
OS   Homo sapiens.
```

XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US019351.
XX
PR 24-AUG-1998; 98US-0097638P.
PR 24-AUG-1998; 98US-0097659P.
PR 09-SEP-1998; 98US-0099618P.
PR 28-SEP-1998; 98US-0102092P.
PR 25-NOV-1998; 98US-0109978P.
PR 23-DEC-1998; 98US-0113645P.
PR 23-DEC-1998; 98US-0113646P.
PR 23-AUG-1999; 99US-00379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding them,
PT useful for treating neurodegenerative disorders, autoimmune diseases and
PT cancer.
XX
PS Claim 73; Page 322-325; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
CC secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
CC activity; cell proliferation; differentiation; immune modulation;
CC haematopoiesis regulation; tissue growth activity; activin/inhibin
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; anti-inflammatory activity; and tumour inhibition activity. The
CC proteins may be administered to patients as vaccines, and the nucleotides
CC may be used as part of a gene therapy regime. Diseases or conditions that
CC may be treated using the proteins or nucleotides of the invention include
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
CC allergic reactions such as asthma and anaemia. They may also be used for
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
CC activity may additionally be useful as contraceptives. Nucleic acid
CC sequences of the invention may be used in chromosome mapping, and as a
CC source of diagnostic primers and probes. The present sequence represents
CC one of the 40 proteins of the invention
XX
SQ Sequence 893 AA;

Query Match 100.0%; Score 931; DB 3; Length 893;
Best Local Similarity 100.0%; Pred. No. 4.4e-92;

```
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 764

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 824

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 884

Qy        181 IPGLKRKAE 189
              |||||||||
Db        885 IPGLKRKAE 893


RESULT 2
ABU11573
ID   ABU11573 standard; protein; 983 AA.
XX
AC   ABU11573;
XX
DT   12-FEB-2003  (first entry)
XX
DE   Human MDDT polypeptide SEQ ID 520.
XX
KW   MDDT; human; disease detection and treatment molecule polypeptide;
KW   anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW   haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW   gene therapy; protein replacement therapy; cell proliferative disorder;
KW   cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW   anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW   Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW   psoriasis; hepatitis.
XX
OS   Homo sapiens.
XX
PN   WO200279449-A2.
XX
PD   10-OCT-2002.
XX
PF   27-MAR-2002; 2002WO-US009944.
XX
PR   28-MAR-2001; 2001US-0279619P.
PR   29-MAR-2001; 2001US-0280067P.
PR   29-MAR-2001; 2001US-0280068P.
PR   16-MAY-2001; 2001US-0291280P.
PR   17-MAY-2001; 2001US-0291829P.
PR   17-MAY-2001; 2001US-0291849P.
PR   19-JUN-2001; 2001US-0299428P.
PR   20-JUN-2001; 2001US-0299776P.
PR   20-JUN-2001; 2001US-0300001P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
```

XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR N-PSDB; ABX34563.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 983 AA;

Query Match 100.0%; Score 931; DB 6; Length 983;
Best Local Similarity 100.0%; Pred. No. 5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        795 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 854

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        855 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 914

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 974

Qy        181 IPGLKRKAE 189
              |||||||||
Db        975 IPGLKRKAE 983
```

```
RESULT 3
AAY71311
ID   AAY71311 standard; protein; 1178 AA.
XX
AC   AAY71311;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Human neurite growth inhibitor Nogo.
XX
KW   Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 187
FT                   /label= Unknown
FT   Misc-difference 188
FT                   /label= Unknown
FT   Misc-difference 189
FT                   /label= Unknown
FT   Misc-difference 190
FT                   /label= Unknown
FT   Misc-difference 221
FT                   /label= Unknown
FT   Misc-difference 328
FT                   /label= Unknown
FT   Misc-difference 477
FT                   /label= Unknown
FT   Region          977. .1012
FT                   /note= "Region specifically described in claim 16"
FT   Region          994. .1174
FT                   /note= "Region specifically described in claim 16"
FT   Region          1079. .1114
FT                   /note= "Region specifically described in claim 16"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
```

XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 11; Fig 13; 122pp; English.
XX
CC The present sequence is a human Nogo protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The human Nogo
CC sequence was derived by aligning human expressed sequence tags (ESTs)
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments
CC displaying neurite growth inhibitory activity are used in the treatment
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 1178 AA;

Query Match 100.0%; Score 931; DB 3; Length 1178;
Best Local Similarity 100.0%; Pred. No. 6.4e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1049

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1109

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1169

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1170 IPGLKRKAE 1178
```

RESULT 4
AAY56967
ID AAY56967 standard; protein; 1192 AA.

XX
AC AAY56967;
XX
DT 25-APR-2000 (first entry)
XX
DE Human MAGI polypeptide.
XX
KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
KW stroke; cytostatic; cerebroprotective; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200005364-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-GB002360.
XX
PR 22-JUL-1998; 98GB-00016024.
PR 19-JUL-1999; 99GB-00016898.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha RK;
XX
DR WPI; 2000-182693/16.
DR N-PSDB; AAZ56886.
XX
PT Novel polypeptides related to neuroendocrine-specific proteins and
PT polynucleotides useful for diagnosis of various diseases and for
PT treatment of cancer and neurological disorders.
XX
PS Claim 2; Page 20-21; 35pp; English.
XX
CC The invention relates to human MAGI protein, which is similar to
CC neuroendocrine-specific protein. The MAGI protein can be expressed by
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC and antibodies are useful for treating diseases, including neuropathies,
CC spinal injury, neuronal degeneration, neuromuscular disorders,
CC psychiatric disorders and developmental disorders, cancer, stroke and
CC inflammatory disorders. The polynucleoitde is also useful for chromosome
CC localization and for tissue expression studies. The present sequence
CC represents the human MAGI protein
XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 3; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy         121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy         181 IPGLKRKAE 189
                |||||||||
Db        1184 IPGLKRKAE 1192
```

RESULT 5
AAB82349
ID AAB82349 standard; protein; 1192 AA.
XX
AC AAB82349;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human NOGO-A protein.
XX
KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
KW neuromuscular disorder; psychiatric disorder; developmental disorder;
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
KW cerebroprotective; neuroleptic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200136631-A1.
XX
PD 25-MAY-2001.
XX
PF 14-NOV-2000; 2000WO-GB004345.
XX
PR 15-NOV-1999; 99GB-00026995.
PR 24-JAN-2000; 2000GB-00001550.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha R;
XX
DR WPI; 2001-343822/36.
DR N-PSDB; AAF90324.
XX
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.
XX
PS Disclosure; Page 26-27; 25pp; English.
XX
CC The present sequence is that of human NOGO-A. NOGO-A is a previously
CC known splice variant of the human NOGO gene on chromosome 2p21. The
CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It
CC provides NOGO-C polypeptides and polynucleotides, and methods for
CC producing such polypeptides by recombinant techniques. Also disclosed are

CC methods for utilising NOGO-C polypeptides and polynucleotides in the
CC treatment of diseases including neuropathies, spinal injury, brain
CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
CC and developmental disorders. Also provided are methods for identifying
CC agonists and agonists for use in treating conditions associated with NOGO
CC -C imbalance, and diagnostic assays for detecting diseases associated
CC with inappropriate NOGO-C activity or levels
XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 4; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192
```

RESULT 6
AAU04591
ID AAU04591 standard; protein; 1192 AA.
XX
AC AAU04591;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human Nogo protein.
XX
KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasis demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1054. .1119
FT /label= Lumenal_extracellular_domain
FT /note= "This sequence is specifically claimed"

FT Peptide 1055. .1094
FT /label= Pep1
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1064. .1088
FT /label= Pep2
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1074. .1098
FT /label= Pep3
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1084. .1108
FT /label= Pep4
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1095. .1119
FT /label= Pep5
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
XX
PN WO200151520-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001041.
XX
PR 12-JAN-2000; 2000US-0175707P.
PR 26-MAY-2000; 2000US-0207366P.
PR 29-SEP-2000; 2000US-0236378P.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM;
XX
DR WPI; 2001-442138/47.
DR N-PSDB; AAS09453.
XX
PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders.
XX
PS Example 1; Page 101-104; 109pp; English.
XX
CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon
CC growth inhibitor. The invention relates to the use of the nogo receptor,
CC nogo protein, their nucleic acids, vectors expressing them and antibodies
CC against them, to isolate agents which block nogo receptor mediated axonal
CC growth. The agent is useful for treating a central nervous system
CC disorder which is a result of cranial or cerebral trauma, spinal cord
CC injury, stroke or a demyelinating disease selected from multiple
CC sclerosis, monophasis demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC Spongy degeneration, Alexander's disease, Canavan's disease,
CC metachromatic leukodystrophy, viral infection and Krabbe's disease
XX

SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 4; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192
```

RESULT 7
ABG30938
ID ABG30938 standard; protein; 1192 AA.
XX
AC ABG30938;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human NogoA protein.
XX
KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
KW Nogo-associated disease; metastasis.
XX
OS Homo sapiens.
XX
PN WO200257483-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-GB000228.
XX
PR 18-JAN-2001; 2001GB-00001312.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
XX
DR WPI; 2002-599722/64.
DR N-PSDB; ABK90134.

XX
PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
PT providing and monitoring interaction between Nogo and BACE polypeptides.
XX
PS Disclosure; Page 59-62; 68pp; English.
XX
CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the
CC interaction between these polypeptides, and determining if the test agent
CC is a modulator of Nogo or BACE activity. The method is useful in treating
CC acute neuronal injuries, such as spinal or head injury, stroke,
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
CC hypertrophy) of the central nervous system. The BACE polypeptide is
CC useful in screening methods to identify agents that may act as modulators
CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present amino acid sequence represents the human NogoA
CC protein of the invention
XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192
```

RESULT 8
ABP68600
ID ABP68600 standard; protein; 1192 AA.
XX

AC ABP68600;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed protein SEQ ID NO 71.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
DR N-PSDB; ABV94680.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192
```

RESULT 9
ABB81078
ID ABB81078 standard; protein; 1192 AA.
XX
AC ABB81078;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human neurotransmitter receptor protein Nogo-A.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; human; receptor.
XX
OS Homo sapiens.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;

PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86601.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Example; Page 53-56; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the human
CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
CC antigen
XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
                |||||||||
Db       1184 IPGLKRKAE 1192


RESULT 10
ABR59667
ID   ABR59667 standard; protein; 1192 AA.
XX
AC   ABR59667;
XX
DT   22-JUL-2003  (first entry)
XX
DE   Human NogoA protein.
XX
KW   Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
KW   axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
KW   cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
KW   demyelinating disease; multiple sclerosis; monophasic demyelination;
KW   encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.
XX
OS   Homo sapiens.
XX
PN   WO2003031462-A2.
XX
PD   17-APR-2003.
XX
PF   04-OCT-2002; 2002WO-US032007.
XX
PR   06-OCT-2001; 2001US-00972599.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Strittmatter SM;
XX
DR   WPI; 2003-393433/37.
DR   N-PSDB; ACC81048.
XX
PT   New human Nogo receptor polypeptides and nucleic acids, useful for
PT   decreasing inhibition of axonal growth by a central nervous system
PT   neuron, or in treating central nervous system disease, disorder or
PT   injury, e.g. spinal cord injury.
XX
PS   Disclosure; Page 131-135; 148pp; English.
XX
CC   The invention relates to a novel nucleic acid encoding a polypeptide
CC   comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
CC   human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
CC   1-20 conservative amino acid substitutions, and less than a complete CTS
CC   domain, provided that a partial CTS domain, if present, consists of no
CC   more than the first 39 consecutive residues. The nucleic acid of the
CC   invention has neuroprotective activity. The polynucleotide may have a use
CC   in gene therapy. The nucleic acid is useful for decreasing inhibition of
CC   axonal growth by a central nervous system (CNS) neuron. The NgR
```

CC polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-
CC dependent signal transduction in the central nervous system neuron may be
CC used in treating central nervous system disease, disorder or injury, e.g.
CC spinal cord injury. Expression of an NgR protein may be associated with
CC inhibition of axonal regeneration following cranial, cerebral or spinal
CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
CC monophasic demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
CC sequence is used in the exemplification of the invention
XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 6; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192
```

RESULT 11
AAB64514
ID AAB64514 standard; protein; 200 AA.
XX
AC AAB64514;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 28 SEQ ID NO:152.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
KW angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
KW ocular disorder; corneal infection; wound healing; food additive;
KW preservative.
XX
OS Homo sapiens.
XX
PN WO200077255-A1.
XX

PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US014926.
XX
PR 11-JUN-1999; 99US-0138628P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-025337/03.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 566; 593pp; English.
XX
CC The polynucleotide sequences given in AAF32699 to AAF32747 encode the
CC human secreted proteins given in AAB64422 to AAB64470. AAB64471 to
CC AAB64548 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
CC neuroprotective; antibacterial; virucide; fungicide; and
CC ophthalmological. The polynucleotides and polypeptides can be used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. AAF32690 to AAF32698 and
CC AAB64421 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 200 AA;

Query Match 99.7%; Score 928; DB 4; Length 200;
Best Local Similarity 99.5%; Pred. No. 1.3e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 71

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db         72 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 131

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 191

Qy        181 IPGLKRKAE 189
              |||||||||
Db        192 IPGLKRKAE 200
```

RESULT 12
AAW53947
ID AAW53947 standard; protein; 199 AA.
XX
AC AAW53947;
XX
DT 24-JUL-1998 (first entry)
XX
DE Human NSPLP protein A.
XX
KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.
XX
OS Homo sapiens.
XX
PN WO9806841-A2.
XX
PD 19-FEB-1998.
XX
PF 24-JUL-1997; 97WO-US013469.
XX
PR 12-AUG-1996; 96US-00700607.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Au-Young J, Goli SK, Hillman J;
XX
DR WPI; 1998-159533/14.
DR N-PSDB; AAV23695.
XX
PT Human neuro-endocrine-specific protein-like proteins - useful for
PT diagnosis, monitoring and treatment of cancer and neuro-degenerative
PT disease.
XX
PS Claim 1; Page 38; 73pp; English.
XX
CC This sequence is a human neuroendocrine-specific protein-like protein
CC (NSPLP) of the invention. Recombinant cells transformed with the DNA are
CC used to express the NSPLP proteins, which are used to treat cancer and
CC neurodegenerative diseases such as amyotrophic lateral sclerosis. Also
CC antisense nucleic acids and antagonists of NSPLP can be used to inhibit
CC activity of the NSPLP proteins. Antibodies specific for NSPLP are used
CC for diagnosis and monitoring treatment of diseases associated with NSPLP
CC expression, in usual immunoassays, and to isolate NSPLP from natural
CC sources. The NSPLP proteins, or their fragments can also be used in drug
CC screening to identify NSPLP antagonists. The nucleic acid can be used

```
CC   diagnostically and for monitoring treatment (in hybridisation or
CC   amplification assays); to isolate closely related sequences; in gene
CC   therapy for both sense and antisense applications (including use of
CC   ribozymes) and for mapping the natural genomic sequence
XX
SQ   Sequence 199 AA;

  Query Match             99.6%;  Score 927;  DB 2;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-92;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
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Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              ||||||||
Db        192 PGLKRKAE 199


RESULT 13
AAW78313
ID   AAW78313 standard; protein; 199 AA.
XX
AC   AAW78313;
XX
DT   13-APR-1999  (first entry)
XX
DE   Fragment of human secreted protein encoded by gene 69.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9856804-A1.
XX
PD   17-DEC-1998.
XX
PF   11-JUN-1998;   98WO-US012125.
XX
PR   13-JUN-1997;   97US-0049547P.
PR   13-JUN-1997;   97US-0049548P.
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PR 13-JUN-1997; 97US-0049549P.
PR 13-JUN-1997; 97US-0049550P.
PR 13-JUN-1997; 97US-0049566P.
PR 13-JUN-1997; 97US-0049606P.
PR 13-JUN-1997; 97US-0049607P.
PR 13-JUN-1997; 97US-0049608P.
PR 13-JUN-1997; 97US-0049609P.
PR 13-JUN-1997; 97US-0049610P.
PR 13-JUN-1997; 97US-0049611P.
PR 13-JUN-1997; 97US-0050901P.
PR 13-JUN-1997; 97US-0052989P.
PR 08-JUL-1997; 97US-0051919P.
PR 18-AUG-1997; 97US-0055984P.
PR 12-SEP-1997; 97US-0058665P.
PR 12-SEP-1997; 97US-0058668P.
PR 12-SEP-1997; 97US-0058669P.
PR 12-SEP-1997; 97US-0058750P.
PR 12-SEP-1997; 97US-0058971P.
PR 12-SEP-1997; 97US-0058972P.
PR 12-SEP-1997; 97US-0058975P.
PR 02-OCT-1997; 97US-0060834P.
PR 02-OCT-1997; 97US-0060841P.
PR 02-OCT-1997; 97US-0060844P.
PR 02-OCT-1997; 97US-0060865P.
PR 02-OCT-1997; 97US-0061059P.
PR 02-OCT-1997; 97US-0061060P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;
PI Feng P;
XX
DR WPI; 1999-080881/07.
DR N-PSDB; AAX04379.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Disclosure; Page 62; 380pp; English.
XX
CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 86 novel genes and their fragments (nucleic acid sequences:
CC AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 86 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAX04311 for
CC described uses)
XX

SQ Sequence 199 AA;

Query Match 99.6%; Score 927; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              ||||||||
Db        192 PGLKRKAE 199
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RESULT 14
AAB12805
ID AAB12805 standard; protein; 199 AA.
XX
AC AAB12805;
XX
DT 24-NOV-2000 (first entry)
XX
DE Human NSPH protein sequence SEQ ID NO:4.
XX
KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC.
XX
OS Homo sapiens.
XX
PN CN1253180-A.
XX
PD 17-MAY-2000.
XX
PF 30-OCT-1998; 98CN-00121473.
XX
PR 30-OCT-1998; 98CN-00121473.
XX
PA (UYFU-) UNIV FUDAN.
XX
PI Yu L, Zhao Y, Zhang H;
XX
DR WPI; 2000-466537/41.
DR N-PSDB; AAA72981.
XX
PT Specific protein of human neuroendocrine, coding sequence and its
PT preparating process and application.
XX
PS Claim 4; Page 14-15; 21pp; Chinese.
XX

CC The present invention relates to a new member of the human neuroendocrine
CC specific protein family, designated NSPH. The present sequence represents
CC the human NSPH protein
XX
SQ Sequence 199 AA;

Query Match 99.6%; Score 927; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              ||||||||
Db        192 PGLKRKAE 199
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RESULT 15
AAB82348
ID AAB82348 standard; protein; 199 AA.
XX
AC AAB82348;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human NOGO-C protein.
XX
KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
KW neuromuscular disorder; psychiatric disorder; developmental disorder;
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
KW cerebroprotective; neuroleptic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200136631-A1.
XX
PD 25-MAY-2001.
XX
PF 14-NOV-2000; 2000WO-GB004345.
XX
PR 15-NOV-1999; 99GB-00026995.
PR 24-JAN-2000; 2000GB-00001550.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha R;

XX
DR WPI; 2001-343822/36.
DR N-PSDB; AAF90323.
XX
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.
XX
PS Claim 3; Page 25; 25pp; English.
XX
CC The present sequence is that of human NOGO-C, encoded by a novel splice
CC variant of the human NOGO gene on chromosome 2p21. 2 Other splice
CC variants, NOGO-A and NOGO-B, have previously been identified. The
CC invention provides NOGO-C polypeptides and polynucleotides, and methods
CC for producing such polypeptides by recombinant techniques. Also disclosed
CC are methods for utilising NOGO-C polypeptides and polynucleotides in the
CC treatment of diseases including neuropathies, spinal injury, brain
CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
CC and developmental disorders. Also provided are methods for identifying
CC agonists and agonists for use in treating conditions associated with NOGO
CC -C imbalance, and diagnostic assays for detecting diseases associated
CC with inappropriate NOGO-C activity or levels
XX
SQ Sequence 199 AA;

Query Match 99.6%; Score 927; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              ||||||||
Db        192 PGLKRKAE 199
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Search completed: September 29, 2004, 18:14:01
Job time : 17.5871 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 4.69196 Seconds
(without alignments)
2079.581 Million cell updates/sec

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Perfect score: 931
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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	927	99.6	199	2	US-08-700-607-1	Sequence 1, Appli
2	682	73.3	208	2	US-08-700-607-7	Sequence 7, Appli
3	682	73.3	356	2	US-08-700-607-6	Sequence 6, Appli
4	682	73.3	776	2	US-08-700-607-5	Sequence 5, Appli
5	665	71.4	267	2	US-08-700-607-8	Sequence 8, Appli
6	541.5	58.2	168	4	US-09-149-476-563	Sequence 563, App
7	512	55.0	241	2	US-08-700-607-3	Sequence 3, Appli
8	285	30.6	92	4	US-09-149-476-411	Sequence 411, App
9	100	10.7	80	3	US-08-905-223-411	Sequence 411, App
10	89	9.6	468	4	US-08-487-596-8	Sequence 8, Appli
11	89	9.6	468	4	US-08-660-451A-8	Sequence 8, Appli

12	88.5	9.5	1278	4	US-09-462-136-2	Sequence 2, Appli
13	87.5	9.4	592	4	US-09-134-000C-5477	Sequence 5477, Ap
14	87.5	9.4	1051	4	US-09-134-001C-5005	Sequence 5005, Ap
15	85	9.1	414	4	US-08-956-171E-5246	Sequence 5246, Ap
16	83	8.9	744	4	US-09-785-381-1	Sequence 1, Appli
17	83	8.9	744	4	US-09-785-381-3	Sequence 3, Appli
18	82.5	8.9	554	4	US-09-252-991A-27968	Sequence 27968, A
19	81.5	8.8	598	2	US-08-853-659A-53	Sequence 53, Appl
20	81	8.7	970	4	US-09-795-927-7	Sequence 7, Appli
21	80.5	8.6	280	4	US-09-543-681A-6175	Sequence 6175, Ap
22	80.5	8.6	593	4	US-09-328-352-4866	Sequence 4866, Ap
23	79	8.5	993	4	US-08-836-687B-30	Sequence 30, Appl
24	78.5	8.4	446	4	US-09-543-681A-6579	Sequence 6579, Ap
25	78	8.4	292	4	US-09-489-039A-12212	Sequence 12212, A
26	78	8.4	349	4	US-09-198-452A-973	Sequence 973, App
27	77	8.3	154	1	US-08-366-783-5	Sequence 5, Appli
28	77	8.3	424	4	US-09-543-681A-7510	Sequence 7510, Ap
29	77	8.3	614	4	US-09-540-236-2858	Sequence 2858, Ap
30	76.5	8.2	420	4	US-09-134-001C-3805	Sequence 3805, Ap
31	76	8.2	1053	4	US-09-328-352-5058	Sequence 5058, Ap
32	75.5	8.1	397	4	US-09-328-352-7457	Sequence 7457, Ap
33	75.5	8.1	454	4	US-09-904-615-165	Sequence 165, App
34	75	8.1	248	4	US-09-198-452A-1153	Sequence 1153, Ap
35	75	8.1	1421	4	US-09-252-991A-17805	Sequence 17805, A
36	74.5	8.0	390	4	US-09-198-452A-254	Sequence 254, App
37	74	7.9	289	4	US-09-540-236-2019	Sequence 2019, Ap
38	74	7.9	1160	4	US-09-328-352-6826	Sequence 6826, Ap
39	73.5	7.9	208	4	US-09-107-532A-6378	Sequence 6378, Ap
40	73.5	7.9	517	4	US-09-540-236-2403	Sequence 2403, Ap
41	73.5	7.9	720	4	US-09-134-000C-5631	Sequence 5631, Ap
42	73	7.8	231	4	US-09-198-452A-419	Sequence 419, App
43	73	7.8	379	4	US-09-491-577-6	Sequence 6, Appli
44	73	7.8	700	4	US-09-543-681A-4969	Sequence 4969, Ap
45	72.5	7.8	408	4	US-09-107-532A-6198	Sequence 6198, Ap

ALIGNMENTS

```
RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
```

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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  199 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:  Consensus
US-08-700-607-1

  Query Match             99.6%;  Score 927;  DB 2;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-93;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
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Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              ||||||||
Db        192 PGLKRKAE 199


RESULT 2
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;     APPLICANT:  Bandman, Olga
;     APPLICANT:  Au-Young, Janice
;     APPLICANT:  Goli, Surya K.
;     APPLICANT:  Hillman, Jennifer L.
```

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

Query Match 73.3%; Score 682; DB 2; Length 208;
Best Local Similarity 68.4%; Pred. No. 2.6e-66;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
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              |: |||||||||||||::|::|:|::||:| :|||||| ||||   ::   :||||||||
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Qy        183 GLKRKAE 189
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Db        202 GAKRHAE 208
```

RESULT 3
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

Query Match 73.3%; Score 682; DB 2; Length 356;
Best Local Similarity 68.4%; Pred. No. 5.5e-66;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
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Db        170 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 229

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:||||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db        230 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 289
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Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|||||| ||||   ::   :||||||||
Db        290 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 349

Qy        183 GLKRKAE 189
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Db        350 GAKRHAE 356


RESULT 4
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,607
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0114 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  776 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  307307
US-08-700-607-5

  Query Match             73.3%;  Score 682;  DB 2;  Length 776;
  Best Local Similarity   68.4%;  Pred. No. 1.6e-65;
  Matches  128;  Conservative   31;  Mismatches   28;  Indels    0;  Gaps    0;
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Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        590 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db        650 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|||||| ||||   ::   :||||||||
Db        710 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy        183 GLKRKAE 189
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Db        770 GAKRHAE 776
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RESULT 5
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,607
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0114 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  281046
US-08-700-607-8

  Query Match             71.4%;  Score 665;  DB 2;  Length 267;
  Best Local Similarity   67.2%;  Pred. No. 2.6e-64;
  Matches  123;  Conservative   33;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db         73 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|||||:| |||| :: :|||||||
Db        133 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIP 192

Qy        183 GLK 185
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Db        193 GAR 195


RESULT 6
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312

; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,880
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
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; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

; EARLIER FILING DATE: 1997-10-02

Query Match 58.2%; Score 541.5; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 3.7e-51;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

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              :||||  ||::|| :|: |||||||||||||| ||||:|||:|||||:|||: :: :| |
Db          1 MLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy         84 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALI 143
                 | |:|:·|:|  :| : |||||:||||||| || ||: |||||:|||:|||||| :
Db         61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAEL 120

Qy        144 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 189
               :||||::||::: |||||:|:|    |  : |||||:||: |:|||
Db        121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167
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RESULT 7
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  THP1NOB01
;       CLONE:  31870
US-08-700-607-3

  Query Match             55.0%;  Score 512;  DB 2;  Length 241;
  Best Local Similarity   52.4%;  Pred. No. 1e-47;
  Matches   98;  Conservative   35;  Mismatches   34;  Indels   20;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :| ||: |||:|||| ||| :| :|||| ||::|| :|: |||||||||||||| ||||
Db         47 AVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 106

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              :|||:|||||:|||: :: :| |    | |:|: |:|  :| : |||||:||||||| ||
Db        107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
               ||: |||||:|||:|||||| : : |||::| ::                    |: :|
Db        167 FMWLMTYVGAVFNGITLLILAELLIXSVPIVYXKY--------------------KVPSK 206

Qy        181 IPGLKRK 187
               |  ::|
Db        207 TPWNRQK 213


RESULT 8
US-09-149-476-411
; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
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;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13

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;  EARLIER APPLICATION NUMBER: 60/061,060
;  EARLIER FILING DATE: 1997-10-02

  Query Match             30.6%;  Score 285;  DB 4;  Length 92;
  Best Local Similarity   57.1%;  Pred. No. 1.3e-23;
  Matches   52;  Conservative   20;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          90 NSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP 149
               |:|: |:|  :| : |||||:||||||| || ||: |||||:|||:|||||| : :||||
Db           2 NAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61

Qy         150 VIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
               ::||::: |||||:|:|    |  : || :|
Db          62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92


RESULT 9
US-08-905-223-411
; Sequence 411, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  411:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  80 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
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;       TISSUE TYPE:  Brain
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  -78..-1
;       IDENTIFICATION METHOD:  Von Heijne matrix
;       OTHER INFORMATION:  score 6.3
;       OTHER INFORMATION:  seq TLIMLLSWQLSVS/SV
US-08-905-223-411

  Query Match             10.7%;  Score 100;  DB 3;  Length 80;
  Best Local Similarity   57.1%;  Pred. No. 0.0015;
  Matches   20;  Conservative    8;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLS--LTVFSI 33
              :| ||::|||:|||| ||| :| :|||  |:| |:
Db         46 AVHDLIFWRDVKKTGFVFGTTLIMLLSWQLSVSSV 80


RESULT 10
US-08-487-596-8
; Sequence 8, Application US/08487596
; Patent No. 6440681
;  GENERAL INFORMATION:
;     APPLICANT:  Elliot, Kathryn J.
;     APPLICANT:  Ellis, Steven B.
;     APPLICANT:  Harpold, Michael M.
;     TITLE OF INVENTION:  METHODS FOR IDENTIFYING AGONISTS AND
;     TITLE OF INVENTION:  ANTAGONISTS FOR HUMAN NEURONAL
;     TITLE OF INVENTION:  NICOTINIC ACETYLCHOLINE RECEPTORS
;     NUMBER OF SEQUENCES:  18
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Brown, Martin, Haller & McClain
;       STREET:  1660 Union Street
;       CITY:  San Diego
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/487,596
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO US94/02447
;       FILING DATE:  08-MAR-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/149,503
;       FILING DATE:  08-NOV-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/028,031
;       FILING DATE:  08-MAR-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/938,154
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;       FILING DATE:  30-NOV-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/504,455
;       FILING DATE:  03-APR-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie L.
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  6362-9951
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-238-0999
;       TELEFAX:  619-238-0062
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  468 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-487-596-8

  Query Match              9.6%;  Score 89;  DB 4;  Length 468;
  Best Local Similarity   20.9%;  Pred. No. 0.28;
  Matches   40;  Conservative   29;  Mismatches   66;  Indels   56;  Gaps    5;

Qy         24 LLLSLTVFSIV----------SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 70
              :|:||||| :|             :  |:   :: ||:|  :    |    :|   |
Db        288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHHRSSSTHNA 347

Qy         71 RAYL--------------------------ESEVAISEELVQKYSNSALGHVNCTIKEL 103
               | |                          |:|     :  :    :||  :    : :
Db        348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy        104 RRLFLVDDLVDSLKF------AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 157
               :   | ::|:  ||       : :| | :|          |:  : || |||||:
Db        408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS---------IVGSLGLF-VPVIYKWANI 457

Qy        158 QIDHYLGLANK 168
               |  ::| |||
Db        458 LIPVHIGNANK 468


RESULT 11
US-08-660-451A-8
; Sequence 8, Application US/08660451A
; Patent No. 6524789
;  GENERAL INFORMATION:
;    APPLICANT:  Elliott, Kathryn J.
;    APPLICANT:  Harpold, Michael M.
;    TITLE OF INVENTION:  HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;    TITLE OF INVENTION:  RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101-2926
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,451A
;      FILING DATE:  June 7, 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/484,722
;      FILING DATE:  06/07/95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-9370B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-238-0999
;      TELEFAX:  619-238-0062
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-660-451A-8

  Query Match             9.6%;  Score 89;  DB 4;  Length 468;
  Best Local Similarity   20.9%;  Pred. No. 0.28;
  Matches   40;  Conservative   29;  Mismatches   66;  Indels   56;  Gaps    5;

Qy         24 LLLSLTVFSIV----------SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 70
              :|:||||| :|              :  |:   :: ||:|  :    |    :|   |
Db        288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHHRSSSTHNA 347

Qy         71 RAYL--------------------------ESEVAISEELVQKYSNSALGHVNCTIKEL 103
               | |                            |:|     :  :    :||  :    : :
Db        348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy        104 RRLFLVDDLVDSLKF------AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 157
              :   | ::|:  ||       : :| | :|          |:  : || |||||:
Db        408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS---------IVGSLGLF-VPVIYKWANI 457

Qy        158 QIDHYLGLANK 168
              |  ::| |||
Db        458 LIPVHIGNANK 468


RESULT 12
US-09-462-136-2
; Sequence 2, Application US/09462136
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; Patent No. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carstea, et al.
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease
; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-136-2

Query Match 9.5%; Score 88.5; DB 4; Length 1278;
Best Local Similarity 25.7%; Pred. No. 1.3;
Matches 39; Conservative 25; Mismatches 51; Indels 37; Gaps 7;

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Qy          46 SVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 105
               ::||||   : :   : :  :   |       | ||  ::  | : ||||    ||  ||
Db         598 NLTISFTAERSIEDELNRESDSDVF------TVVISYAIMFLYISLALGH----IKSCRR 647

Qy         106 LFLVDD---------LVDSLKFAVLMWVFTYVGALFNGLTLLILALI----------SLF 146
               | |||          |:     |  : ||:|:|     |||::: :|          ::|
Db         648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy         147 SVPVIYERHQ----AQIDHYLGLANKNVKDAM 174
                :   |:| :      :|  ||     |  :|
Db         704 ILVQAYQRDERLQGETLDQQLGRVLGEVAPSM 735
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RESULT 13
US-09-134-000C-5477
; Sequence 5477, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5477
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5477

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  Query Match             9.4%;  Score 87.5;  DB 4;  Length 592;
  Best Local Similarity   20.8%;  Pred. No. 0.56;
  Matches   48;  Conservative   41;  Mismatches   65;  Indels   77;  Gaps   10;

Qy          7 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR----------IYK 55
              :|: :|:        ||  :|  : ||::|   : ||: :|    :           |:|
Db         45 FWKTVKR--------LFRYMSKRMLSIIAV---LVLAIAAVVFQIQTPKVLGQATTEIFK 93

Qy         56 GVIQAIQKSDEGHPFRA----------------YLESEV----------------A 79
              ||::   :  :|    :                  || | |
Db         94 GVMKGAAEMKQGLKITSFPIDFDKIGQILLIVIAMYLISAVFNFLQQVIMTRVSQRTVYE 153

Qy         80 ISEELVQKYSNSALG----HVNCTIKELRRLFLVDDLVDSLK---FAVLMWVFTYVGALF 132
              : :||  | :   :     | |  |   | :  :|::  :|:     ::  : |:|| |:
Db        154 LRQELEAKMNKVPISYYDIHSNGDIMS-RAINDMDNIASTLQQNLTQLITSIVTFVGVLW 212

Qy        133 NGLTL-LILALISLFSVPVIY----------ERHQAQIDHYLGLANKNVKD 172
                ||:   | ||:| :||:            ::| |     ||| |  |::
Db        213 MMLTISWQLTLIALATVPLSLIVVMVVAPRSQKHFAAQQKSLGLLNNQVEE 263


RESULT 14
US-09-134-001C-5005
; Sequence 5005, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5005
;   LENGTH: 1051
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5005

  Query Match             9.4%;  Score 87.5;  DB 4;  Length 1051;
  Best Local Similarity   22.9%;  Pred. No. 1.2;
  Matches   44;  Conservative   35;  Mismatches   68;  Indels   45;  Gaps    8;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV-----TAYIALALLSVTISFRIYKG 56
              :| ||: |:|: | :               ||||:      | ||| | :|:::
Db        380 IVILLFLRNIRTTAI---------------SIVSIPMSILIALIALKLSNVSLNILTLGA 424

Qy         57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYS--NSALGHVNCTIKELRRLF---LVDD 111
              :  || :          ::  : : | : :: |  |  |   |  |   | :|   :
Db        425 LTVAIGR---------VIDDSIVVVENIFRRLSDPNEKLKGENLIISATREVFKPIMSST 475

Qy        112 LVDSLKFAVLMWVFTYVGALFN----GLTLLILA--LISLFSVPVIYERHQAQIDHYLGL 165
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              ||  : |  |::|   || :|      :|  :||  |:|:  || :            |:
Db        476 LVTIVVFLPLVFVSGSVGEMFRPFALAITFSLLASLLVSITLVPSLGATFFKN-----GV 530

Qy        166 ANKNVKDAMAKI 177
               |:  |: :  :
Db        531 KNREQKEGLGTV 542


RESULT 15
US-08-956-171E-5246
; Sequence 5246, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 5246:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 414 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5246:
```

US-08-956-171E-5246

Query Match 9.1%; Score 85; DB 4; Length 414;
Best Local Similarity 21.8%; Pred. No. 0.63;
Matches 42; Conservative 36; Mismatches 75; Indels 40; Gaps 7;

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Qy          2 VVDLLYWRDIKKTGV-VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :| ||: |:|: | : :    | ||::|           ||| |  |:::      :  |
Db          3 IVILLFLRNIRTTAISIISIPLSLLMAL-----------IALKLSDVSLNILTLGALTVA 51

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNS--ALGHVNCTIKELRRLF---LVDDLVDS 115
              | :          ::  : : | : :: ::|   |   |  |     :|   :   ||
Db         52 IGR---------VIDDSIVVVENIYRRLTDSEEQLKGENLIISATTEVFKPIMSSTLVTI 102

Qy        116 LKFAVLMWVFTYVGALFN------GLTLLILALISLFSVPVI---------YERHQAQIDH 161
              : |  |::|   || :|         :||   |:|:  || :          :|   |
Db        103 IVFLPLVFVSGSVGEMFRPFALAIAFSLLASLLVSITLVPALAATLFKKGVKRRNKQHQE 162

Qy        162 YLGLANKNVKDAM 174
               ||: :   |  :
Db        163 GLGVVSTTYKKVL 175
```

Search completed: September 29, 2004, 18:21:05
Job time : 5.69196 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 4.62587 Seconds
(without alignments)
3930.111 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	682	73.3	208	2	I60904	neuroendocrine-spe
2	682	73.3	776	2	A46583	neuroendocrine-spe
3	665	71.4	267	2	A60021	tropomyosin-relate
4	335	36.0	2484	2	T26216	hypothetical prote
5	335	36.0	2607	2	T26215	hypothetical prote
6	334	35.9	222	2	T26213	hypothetical prote
7	191	20.5	255	2	E84899	hypothetical prote
8	182	19.5	271	2	T13013	hypothetical prote
9	163	17.5	275	2	T05595	hypothetical prote
10	147	15.8	393	2	S67763	probable membrane
11	144.5	15.5	242	2	B85016	hypothetical prote
12	131	14.1	183	2	A84527	hypothetical prote
13	127.5	13.7	295	2	S59439	probable membrane

14	124	13.3	206	2	T01153	probable seed matu
15	109.5	11.8	264	2	T47948	hypothetical prote
16	104.5	11.2	203	2	T47571	hypothetical prote
17	95	10.2	288	2	B90043	conserved hypothet
18	94.5	10.2	458	2	A72258	hypothetical prote
19	93	10.0	160	2	C84422	hypothetical prote
20	92.5	9.9	527	2	A84645	probable cytochrom
21	88.5	9.5	405	2	H71692	hypothetical prote
22	88	9.5	224	2	D71915	hydrogenase, cytoc
23	87.5	9.4	296	2	S46018	probable membrane
24	85.5	9.2	442	2	C75057	hypothetical prote
25	85.5	9.2	823	2	H83724	hypothetical prote
26	85.5	9.2	1065	2	E69795	acriflavin resista
27	85	9.1	224	1	A64599	hydrogenase (EC 1.
28	85	9.1	459	2	G86264	F3F19 hypothetical
29	85	9.1	468	2	A38223	nicotinic acetylch
30	85	9.1	1055	2	H90023	hypothetical prote
31	84.5	9.1	151	2	G96705	unknown protein, 7
32	84.5	9.1	457	2	H85095	hypothetical prote
33	84.5	9.1	464	2	C70414	NADH2 dehydrogenas
34	84.5	9.1	677	2	F95232	immunity protein,
35	84.5	9.1	680	2	H98096	conserved hypothet
36	84	9.0	299	2	B69155	hypothetical prote
37	82.5	8.9	570	2	S52765	secD protein - Str
38	82.5	8.9	955	2	T33040	hypothetical prote
39	82	8.8	589	2	F64201	transport ATP-bind
40	81.5	8.8	324	2	AE1700	phospho-N-acetylmu
41	81.5	8.8	369	2	H90587	hypothetical prote
42	81.5	8.8	598	2	T14886	leukotoxin express
43	81.5	8.8	822	2	T41622	probable ABC trans
44	81.5	8.8	937	2	T41400	probable peroxisom
45	81	8.7	537	2	G82873	conserved hypothet

ALIGNMENTS

RESULT 1
I60904
neuroendocrine-specific protein C - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: I60904
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.
J. Biol. Chem. 268, 13439-13447, 1993
A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.
A;Reference number: A46583; MUID:93293865; PMID:7685762
A;Accession: I60904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-208 <RES>
A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311
C;Genetics:
A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

  Query Match 73.3%; Score 682; DB 2; Length 208;
  Best Local Similarity 68.4%; Pred. No. 3.3e-54;
  Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

```
Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         22 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||
Db         82 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 141

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::|||:| :|||||| |||| ::  :||||||||
Db        142 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 201

Qy        183 GLKRKAE 189
              | || ||
Db        202 GAKRHAE 208
```

RESULT 2
A46583
neuroendocrine-specific protein, splice form A - human
N;Contains: neuroendocrine-specific protein, splice form B
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: A46583; I60903
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.
J. Biol. Chem. 268, 13439-13447, 1993
A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.
A;Reference number: A46583; MUID:93293865; PMID:7685762
A;Accession: A46583
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-776 <ROE1>
A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307
A;Accession: I60903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

  Query Match 73.3%; Score 682; DB 2; Length 776;
  Best Local Similarity 68.4%; Pred. No. 1.5e-53;
  Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        590 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db        650 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|||||| ||||   ::   :||||||||
Db        710 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy        183 GLKRKAE 189
              | || ||
Db        770 GAKRHAE 776
```

RESULT 3
A60021
tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C;Accession: A60021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an
alpha-tropomyosin probe but does not show homology in amino acid sequence.

```
  Query Match             71.4%;  Score 665;  DB 2;  Length 267;
  Best Local Similarity   67.2%;  Pred. No. 1.5e-52;
  Matches  123;  Conservative   33;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db         73 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :||||:| ||||   ::   :||||||||
Db        133 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIP 192

Qy        183 GLK 185
              | :
Db        193 GAR 195
```

RESULT 4
T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26216
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2484 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3c
A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

  Query Match 36.0%; Score 335; DB 2; Length 2484;
  Best Local Similarity 33.7%; Pred. No. 1.1e-21;
  Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

```
Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:|::|||| ||: :|   :| :|  |  : :::|  |  |  |     ||::| |   |
Db       2289 VLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI 2348

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              :|:|  |||   |  :: : :| |   ::  : |  |   :|::|  |:  ::|:|| ::
Db       2349 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLV 2408

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              :|  ||: : |:| || || |: :|||| :|| :|  || :|   : ::|:    |  |:
Db       2409 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 2468

Qy        182 PGLK 185
              | |:
Db       2469 PFLR 2472
```

RESULT 5
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26215
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2607 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3a
A;Map position: 5

```
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

  Query Match             36.0%;  Score 335;  DB 2;  Length 2607;
  Best Local Similarity   33.7%;  Pred. No. 1.2e-21;
  Matches   62;  Conservative   46;  Mismatches   76;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:|::|||| ||: :|   :| :|  |  : :::|  |  |  |     ||::| |   |
Db       2412 VLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI 2471

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              :|:|  |||   |  :: : :| |   ::  : |  |   :|::|  |:  ::|:|| ::
Db       2472 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLV 2531

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              :|  ||: : |:| || || |: :|||| :|| :|  || :|   : ::|:    |  |:
Db       2532 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 2591

Qy        182 PGLK 185
              | |:
Db       2592 PFLR 2595


RESULT 6
T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

  Query Match             35.9%;  Score 334;  DB 2;  Length 222;
  Best Local Similarity   33.2%;  Pred. No. 8.6e-23;
  Matches   61;  Conservative   47;  Mismatches   76;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ::|::|||| ||: :|   :| :|  |  : :::|  |  |  |     ||::| |   |
Db         27 ILDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI 86

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              :|:|  |||   |  :: : :| |   ::  : |  |   :|::|  |:  ::|:|| ::
Db         87 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLV 146

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
```

```
              :|  ||: : |:| || || |: :|||| :|| :|  || :|   : ::|:    |  |:
Db        147 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 206

Qy        182 PGLK 185
              | |:
Db        207 PFLR 210


RESULT 7
E84899
hypothetical protein At2g46170 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84899
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,
G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,
C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84899
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <STO>
A;Cross-references: GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g46170
A;Map position: 2

  Query Match             20.5%;  Score 191;  DB 2;  Length 255;
  Best Local Similarity   27.9%;  Pred. No. 8e-10;
  Matches   55;  Conservative   40;  Mismatches   78;  Indels   24;  Gaps    6;

Qy          4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:  ||| | :| | |   ::::|  |  : ::|:  :|::  |       ::      |
Db         70 DVFLWRDKKLSGAVLGVATAIWVLFELVEYHLLSLLCHISILALG---GLFLWSNAHTLI 126

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
               |:    |       |: : ||     ::|    :|     || : |  ||   |   |
Db        127 NKTSPQIP-------EIHVPEEAFLVVASSLRNELNQAFVILRSIALGRDLKKFLMVVVG 179

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM------- 174
              :|: : ||  || |||: :  : | :||::||:|: ::|    || | :|:
Db        180 LWIISVVGNWFNFLTLVYICFVILHTVPMLYEKHEDKVD---PLAEKAMKELQKQYVVFD 236

Qy        175 AKIQAKIP--GLKRKAE 189
               |: :|||   || ||:
Db        237 EKVLSKIPIASLKAKAK 253


RESULT 8
T13013
```

hypothetical protein F8L21.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999
C;Accession: T13013
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17587
A;Accession: T13013
A;Molecule type: DNA
A;Residues: 1-271 <BEV>
A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.10
A;Experimental source: cultivar Columbia; BAC clone F8L21
C;Genetics:
A;Gene: ATSP:F8L21.10
A;Map position: 4
A;Introns: 85/1; 145/2; 192/3; 216/1

  Query Match 19.5%; Score 182; DB 2; Length 271;
  Best Local Similarity 26.1%; Pred. No. 5.6e-09;
  Matches 47; Conservative 42; Mismatches 79; Indels 12; Gaps 3;

```
Qy          4 DLLYWRDIKKTGVVFGAS--LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:  |:| | :| ||| :   ::|  |  : ::::  :: :  |:|     ::      |
Db         87 DIFMWKDKKMSGGVFGGATVAWVLFELMEYHLLTLLCHVMIVALAVLF---LWSNATMFI 143

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
               ||    |       || | || : : ::     :|  |  || :    |:   |
Db        144 HKSPPKIP-------EVHIPEEPLLQLASGLRIEINRGISSLREIASGRDIKKFLSAIAG 196

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              :|| : :|  :: |||  :||: ||:||: |:::: ::| |   |   :|   | : ||:
Db        197 LWVLSILGGCYSFLTLAYIALVLLFTVPLFYDKYEDKVDSYGEKAMAELKKQYAVLDAKV 256
```

RESULT 9
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05595
R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15419
A;Accession: T05595
A;Molecule type: DNA
A;Residues: 1-275 <BEV>
A;Cross-references: EMBL:AL035394
A;Experimental source: cultivar Columbia; BAC clone F9D16
C;Genetics:
A;Map position: 4
A;Introns: 89/1; 149/2; 196/3; 220/1
A;Note: F9D16.100

  Query Match 17.5%; Score 163; DB 2; Length 275;
  Best Local Similarity 26.0%; Pred. No. 2.9e-07;

```
  Matches   50;  Conservative   42;  Mismatches   82;  Indels   18;  Gaps    5;

Qy          4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:  |:: | :| | |   : :::  |  : ::::  :: : :|:|     ::      |
Db         91 DIFMWKNKKMSGGVLGGATAAWVVFELMEYHLLTLLCHVMIVVLAVLF---LWSNATMFI 147

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
               ||    |       || | || : : ::     :|     || :    ||   |
Db        148 NKSPPKIP-------EVHIPEEPILQLASGLRIEINRGFSSLREIASGRDLKKFLIAIAG 200

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA----KI 177
              :|| : :|  || |||  :||: ||:||: |:::: ::|     |   :|   |    |:
Db        201 LWVLSILGGCFNFLTLAYIALVLLFTVPLAYDKYEDKVDPLGEKAMIELKKQYAVLDEKV 260

Qy        178 QAKIP--GLKRK 187
              :|||   || |
Db        261 LSKIPLGPLKNK 272


RESULT 10
S67763
probable membrane protein YDL204w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D1062
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67763
R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67756
A;Accession: S67763
A;Molecule type: DNA
A;Residues: 1-393 <SCH>
A;Cross-references: EMBL:Z74252; NID:g1431337; PID:e253109; PID:g1431338;
GSPDB:GN00004; MIPS:YDL204w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL204w
A;Cross-references: SGD:S0002363
A;Map position: 4L
C;Keywords: transmembrane protein
F;50-66/Domain: transmembrane #status predicted <TM1>
F;150-166/Domain: transmembrane #status predicted <TM2>

  Query Match           15.8%;  Score 147;  DB 2;  Length 393;
  Best Local Similarity  27.0%;  Pred. No. 1.2e-05;
  Matches   47;  Conservative   34;  Mismatches   51;  Indels   42;  Gaps    5;

Qy          5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS 64
              |:|| :  |:|  | |:|  || |   :::||   |  :|  :
Db         33 LIYWTNPSKSGASFAATLVSLLILRNVNVISVLLKIGYMVLFTS---------------- 76

Qy         65 DEGHPFRAYLESEVAISEELVQKY----SNSALG----HVNCTIKELRRLFLVDDLVDSL 116
                   |   | ::|   : :| ::    |   :|    |::   :|| ||  ::| :  |
Db         77 -----FAVELSTKVLFDKGVVSRFGMQESPDLVGVLKPHID---RELDRLPALEDRIRKL 128

Qy        117 KFA----------VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQID 160
               ||          | ::    : |:|:  |:||:  | |::||:||:| ||:||
```

```
Db        129 VFAHRTRNNFTIGVSLYFLHGLFAIFSMNTVLIMTTIFLYTVPLIYDRKQARID 182
```

RESULT 11
B85016
hypothetical protein AT4g01230 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: B85016
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor, Washington University in St Louis and PE Biosystems Arabidopsis Sequencing Consortium.
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <STO>
A;Cross-references: GB:NC_001268; NID:g7267620; PIDN:CAB80932.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g01230
A;Map position: 4

```
  Query Match             15.5%;  Score 144.5;  DB 2;  Length 242;
  Best Local Similarity   24.7%;  Pred. No. 1.2e-05;
  Matches   47;  Conservative   47;  Mismatches   67;  Indels   29;  Gaps    6;

Qy          4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIV-------SVTAYIALALLSVTISFRIYKG 56
              |:| ||| | |       | || ::||  ::        :|:    ::| : :|| ::
Db         70 DVLLWRDKKVT-------LGLLSAVTVIWLLFGFGGRRLLTSLCRGSILFLLLSF-LWS- 120

Qy         57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 116
                 |: || |          :: | |: : : :::    :||    || : |  |: : :
Db        121 --NALNKSPEN-------MMDIYIPEKPLLQAASAMTFELNCAFATLRSIALERDIKNFV 171

Qy        117 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLA----NKNVKD 172
                : :|: : :|  |: |:|| :  : : :||::||::: :||     |     |: :
Db        172 MAVIGLWLVSVIGNWFSFLSLLYICFVLIHTVPMLYEKYEDEIDPIAEKAVIEMKKHYQV 231

Qy        173 AMAKIQAKIP 182
                ||  :|||
Db        232 FEAKFLSKIP 241
```

RESULT 12
A84527
hypothetical protein At2g15280 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84527
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,

G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
A;Cross-references: GB:AE002093; NID:g4662633; PIDN:AAD26905.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g15280
A;Map position: 2

Query Match 14.1%; Score 131; DB 2; Length 183;
Best Local Similarity 24.0%; Pred. No. 0.00014;
Matches 43; Conservative 38; Mismatches 80; Indels 18; Gaps 4;

```
Qy          8 WRDIKKTGVVFGAS-----LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              |:: :   :: |::     ||     : |  |     :   |||| | |   |  |
Db          2 WKNRRGGFLLLGSTTLLWFLFEKCGYSFFPFV-----VNTQLLSVVILFLWAKSAI---- 52

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
               :   |    ||    |:|| |   :::    :|  :   | :::  :     : :|::
Db         53 LFNRPMPQLPNLE----ITEEFVFMVADAIRVWINTVLAVAREIYVGRNAKQLFRVSVVL 108

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              |  ::||   | ||:| | ::    :| :|||:|  ||  | | :: ::    ||  ::
Db        109 WTVSFVGNFLNFLTILYLGVVLSLLIPFLYERYQDLIDEKLSLTHRVIQTQYRKIDERL 167
```

RESULT 13
S59439
probable membrane protein YDR233c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9934.17c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59439
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
A;Molecule type: DNA
A;Residues: 1-295 <MUR>
A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004; MIPS:YDR233c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 13.7%; Score 127.5; DB 2; Length 295;

```
  Best Local Similarity   21.6%;  Pred. No. 0.0005;
  Matches   45;  Conservative   43;  Mismatches   69;  Indels   51;  Gaps    5;

Qy          4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQK 63
              ||| ||:  :||  || ||  || |   ::::    :|  :|  |       | |: :
Db         22 DLLLWRNPVQTGKYFGGSLLALLILKKVNLITFFLKVAYTILFTT-------GSIEFV-- 72

Qy         64 SDEGHPFRAYLESEVAISEELVQKY--------SNSALGHVNCTIKEL-------RRLFL 108
                        |:: : : |: ||        :     |::  :|:|       |:
Db         73 ------------SKLFLGQGLITKYGPKECPNIAGFIKPHIDEALKQLPVFQAHIRKTVF 120

Qy        109 VDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQID-------- 160
                 : | || :::     : |:  |:: :| |  |::|||  :: :||
Db        121 AQVPKHTFKTAVALFLLHKFFSWFSIWTIVFVADIFTFTLPVIYHSYKHEIDATVAQGVE 180

Qy        161 -------HYLGLANKNVKDAMAKIQAKI 181
                    :  :| :  |  : |:::|:
Db        181 ISKQKTQEFSQMACEKTKPYLDKVESKL 208
```

RESULT 14
T01153
probable seed maturation protein [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F27L4.17
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01153; T02426; C84627
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A;Reference number: Z14198
A;Accession: T01153
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <ROU>
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242725
A;Experimental source: cultivar Columbia
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.
A;Reference number: Z14658
A;Accession: T02426
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <RO2>
A;Cross-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17096.1; PID:g3152617
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84627
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Cross-references: GB:AE002093; NID:g3152617; PIDN:AAC17096.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g23640; F26B6.29; F27L4.17
A;Map position: 2
A;Introns: 14/1; 76/2; 147/1
C;Superfamily: Arabidopsis thaliana hypothetical protein F27L4.17

Query Match 13.3%; Score 124; DB 2; Length 206;
Best Local Similarity 24.4%; Pred. No. 0.00069;
Matches 48; Conservative 44; Mismatches 75; Indels 30; Gaps 8;

```
Qy          2 VVDLLYWRDIKK--TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
              | |:  ||  |   : ::   | ::|||   |: ::: ::| :|::|:     ::  :::
Db         16 VEDIYLWRRKKLAFSTLLVSTSTWILLSFYGFTTITIVSWIGIAVVSMIF---LWGSLLR 72

Qy         60 AIQKSDEGHPFRAYLESEVA---ISEELVQKYSNSALGHVNCTI---KELRRLFLVDDLV 113
               : |          :| |::   :||| | :   |      | :   : :| :| |
Db         73 LLSK----------VEPELSGLEVSEEFVVETVRS------CRMLMEEMVRWMFRVGAES 116

Qy        114 DSLKFA--VL-MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNV 170
               :   ||  ||  |: : :| | :  | | : |:   :|| ::| :  ||  :||
Db        117 EWFVFARTVLGFWILSRIGNLLDFHTCLFIGLVMGLTVPKLWEEYGDQIQKHLGSLKDKS 176

Qy        171 KDAMAKIQAKIPGLKRK 187
              | |      ||  :| |
Db        177 KGAYNTTHEKILEMKNK 193
```

RESULT 15
T47948
hypothetical protein F2A19.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47948
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Accession: T47948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <DEH>
A;Cross-references: EMBL:AL132962
A;Experimental source: cultivar Columbia; BAC clone F2A19
C;Genetics:
A;Map position: 3
A;Introns: 68/1; 128/2; 164/1; 210/1
A;Note: F2A19.160

```
  Query Match             11.8%;  Score 109.5;  DB 2;  Length 264;
  Best Local Similarity   25.2%;  Pred. No. 0.019;
  Matches   55;  Conservative   37;  Mismatches   69;  Indels   57;  Gaps   14;

Qy          4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYI------ALALLSVTISFRIYK 55
              |:  ||| | :  | |   ::::|  |  : :|:  :|      || |||   :| : |
Db         70 DVFLWRDKKLSASVLGVATAIWVLFELVEYHFLSLVCHILIFALAALFLLSNAHAF-MNK 128

Qy         56 GVIQ-----AIQKSDEG------HPFRAYLESEVAISEELVQK-YSN-SALGHVNCTIKE 102
              |          :::: |      |  |  ||    || ||:|  |   | :| |  |
Db        129 GTFPYDCFCTEKRAEPGLCYFKEHCLRKGLEE---ISHELIQSTYETFSIMGFVTRT--- 182

Qy        103 LRRLFLVDDLVDSLKFAVL--MWVFTYVGALFNG--LTLLILALISLFSVPVIYERHQAQ 158
                        |:   :    |    :|    |  : ||    : | :||::||:|: :
Db        183 ------------SIYIGISGGFWAVDNLGC---GKLVQLLDSCFVVLHTVPMLYEKHEDK 227

Qy        159 IDHYLGLANKNVKDAM-------AKIQAKIPGLKRKAE 189
              :|    :| | :|:          |: :|:|    ||:
Db        228 VD---PVAEKTLKELKKHYMVFDEKVLSKLPVASLKAK 262


Search completed: September 29, 2004, 18:16:05
Job time : 6.62587 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:16:15 ; Search time 20.2878 Seconds
(without alignments)
2997.869 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	931	100.0	1192	9	US-09-789-386-2	Sequence 2, Appli
2	931	100.0	1192	9	US-09-758-140-6	Sequence 6, Appli
3	931	100.0	1192	9	US-09-893-348-23	Sequence 23, Appl
4	931	100.0	1192	9	US-09-972-599A-6	Sequence 6, Appli
5	931	100.0	1192	12	US-10-267-502-429	Sequence 429, App
6	931	100.0	1192	14	US-10-060-036-71	Sequence 71, Appl
7	931	100.0	1192	16	US-10-327-213-9	Sequence 9, Appli
8	931	100.0	1192	16	US-10-466-258-9	Sequence 9, Appli
9	927	99.6	199	9	US-09-893-348-25	Sequence 25, Appl
10	927	99.6	199	12	US-10-660-946-1	Sequence 1, Appli
11	927	99.6	373	9	US-09-789-386-6	Sequence 6, Appli
12	927	99.6	373	9	US-09-765-205-6	Sequence 6, Appli
13	927	99.6	373	9	US-09-893-348-24	Sequence 24, Appl
14	927	99.6	373	12	US-10-408-967-8	Sequence 8, Appli
15	927	99.6	373	14	US-10-060-036-72	Sequence 72, Appl
16	927	99.6	373	16	US-10-466-258-4	Sequence 4, Appli
17	924	99.2	1192	12	US-10-408-967-7	Sequence 7, Appli
18	920	98.8	199	12	US-10-408-967-9	Sequence 9, Appli
19	918	98.6	199	12	US-09-978-360A-467	Sequence 467, App
20	908	97.5	1163	9	US-09-893-348-18	Sequence 18, Appl
21	905	97.2	379	14	US-10-205-194-164	Sequence 164, App
22	904.5	97.2	1163	12	US-10-267-502-431	Sequence 431, App
23	904	97.1	199	9	US-09-893-348-21	Sequence 21, Appl
24	904	97.1	360	9	US-09-893-348-20	Sequence 20, Appl
25	886	95.2	199	16	US-10-466-258-11	Sequence 11, Appl
26	682	73.3	208	12	US-10-660-946-7	Sequence 7, Appli
27	682	73.3	356	12	US-10-660-946-6	Sequence 6, Appli
28	682	73.3	776	12	US-10-660-946-5	Sequence 5, Appli
29	682	73.3	776	12	US-10-267-502-430	Sequence 430, App
30	681	73.1	777	14	US-10-205-219-93	Sequence 93, Appl
31	681	73.1	780	12	US-10-267-502-432	Sequence 432, App
32	665	71.4	267	12	US-10-660-946-8	Sequence 8, Appli
33	665	71.4	267	14	US-10-205-194-127	Sequence 127, App
34	624.5	67.1	236	9	US-09-729-674-20	Sequence 20, Appl
35	624.5	67.1	236	9	US-09-765-205-26	Sequence 26, Appl
36	624.5	67.1	236	12	US-10-408-967-2	Sequence 2, Appli
37	624.5	67.1	266	12	US-10-276-774-2330	Sequence 2330, Ap
38	624.5	67.1	269	14	US-10-106-698-6222	Sequence 6222, Ap
39	619.5	66.5	593	15	US-10-108-260A-2892	Sequence 2892, Ap
40	541.5	58.2	168	10	US-09-809-391-563	Sequence 563, App
41	541.5	58.2	168	10	US-09-882-171-563	Sequence 563, App
42	541.5	58.2	168	12	US-10-164-861-563	Sequence 563, App
43	520	55.9	222	12	US-10-267-502-428	Sequence 428, App
44	512	55.0	241	12	US-10-660-946-3	Sequence 3, Appli
45	508.5	54.6	234	12	US-10-424-599-200840	Sequence 200840,

ALIGNMENTS

RESULT 1
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
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Db       1184 IPGLKRKAE 1192
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RESULT 2
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29

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;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-758-140-6

  Query Match             100.0%;  Score 931;  DB 9;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-86;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192


RESULT 3
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 1192
;   TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-893-348-23

  Query Match 100.0%; Score 931; DB 9; Length 1192;
  Best Local Similarity 100.0%; Pred. No. 1.6e-86;
  Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192
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RESULT 4
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-972-599A-6

  Query Match 100.0%; Score 931; DB 9; Length 1192;
  Best Local Similarity 100.0%; Pred. No. 1.6e-86;
  Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
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Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
                |||||||||
Db       1184 IPGLKRKAE 1192


RESULT 5
US-10-267-502-429
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jaeseob
;  APPLICANT:  Galant, Ron
;  TITLE OF INVENTION: Obesity Linked Genes
;  FILE REFERENCE: LSD-07416
;  CURRENT APPLICATION NUMBER: US/10/267,502
;  CURRENT FILING DATE:  2003-01-27
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-267-502-429

  Query Match             100.0%;  Score 931;  DB 12;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-86;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
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Db       1184 IPGLKRKAE 1192


RESULT 6
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US-10-060-036-71
; Sequence 71, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71

Query Match 100.0%; Score 931; DB 14; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
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Db       1184 IPGLKRKAE 1192
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RESULT 7
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20

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;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-327-213-9

  Query Match             100.0%;  Score 931;  DB 16;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-86;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
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Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192


RESULT 8
US-10-466-258-9
; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
;  APPLICANT: GLAXO GROUP LIMITED
;  TITLE OF INVENTION: ASSAY
;  FILE REFERENCE: P80966 GCW
;  CURRENT APPLICATION NUMBER: US/10/466,258
;  CURRENT FILING DATE:  2003-07-15
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-466-258-9

  Query Match             100.0%;  Score 931;  DB 16;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-86;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
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Db       1184 IPGLKRKAE 1192
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RESULT 9
US-09-893-348-25
; Sequence 25, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-25

Query Match 99.6%; Score 927; DB 9; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-87;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191
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Qy        182 PGLKRKAE 189
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Db        192 PGLKRKAE 199


RESULT 10
US-10-660-946-1
; Sequence 1, Application US/10660946
; Publication No. US20040063131A1
;   GENERAL INFORMATION:
;        APPLICANT: Bandman, Olga
;                   Au-Young, Janice
;                   Goli, Surya K.
;                   Hillman, Jennifer L.
;        TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Incyte Pharmaceuticals, Inc.
;             STREET: 3174 Porter Drive
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: U.S.
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 1.5
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/660,946
;             FILING DATE: 12-Sep-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/228,213A
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/700,607
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Billings, Lucy J.
;             REGISTRATION NUMBER: 36,749
;             REFERENCE/DOCKET NUMBER: PF-0114 US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-855-0555
;             TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 199 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        IMMEDIATE SOURCE:
;             LIBRARY: <Unknown>
;             CLONE: Consensus
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-660-946-1
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  Query Match             99.6%;  Score 927;  DB 12;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-87;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
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Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
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Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
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Db        192 PGLKRKAE 199


RESULT 11
US-09-789-386-6
; Sequence 6, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
;  APPLICANT: MICHALOVICH, DAVID
;  APPLICANT:  PRINJHA, RABINDER KUMAR
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP-30165-C1
;  CURRENT APPLICATION NUMBER: US/09/789,386
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: U.K. 9916898.1
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: U.K. 9816024.5
;  PRIOR FILING DATE: 1998-07-22
;  PRIOR APPLICATION NUMBER: US 09/359,208
;  PRIOR FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-789-386-6

  Query Match             99.6%;  Score 927;  DB 9;  Length 373;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-87;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
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Db        186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 245

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305
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Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
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Db        306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy        182 PGLKRKAE 189
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Db        366 PGLKRKAE 373
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RESULT 12
US-09-765-205-6
; Sequence 6, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Li
;  TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
;  FILE REFERENCE: 1458.004/200130.449
;  CURRENT APPLICATION NUMBER: US/09/765,205
;  CURRENT FILING DATE:  2001-01-17
;  PRIOR APPLICATION NUMBER: US/09/212,440
;  PRIOR FILING DATE: 1998-12-16
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: human
US-09-765-205-6

  Query Match             99.6%;  Score 927;  DB 9;  Length 373;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-87;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 245

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy        182 PGLKRKAE 189
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Db        366 PGLKRKAE 373
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RESULT 13
US-09-893-348-24
; Sequence 24, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
```

```
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-893-348-24

  Query Match             99.6%;  Score 927;  DB 9;  Length 373;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-87;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 245

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy        182 PGLKRKAE 189
              ||||||||
Db        366 PGLKRKAE 373


RESULT 14
US-10-408-967-8
; Sequence 8, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia & Upjohn Company
;  APPLICANT:  Yan, Riqiang
;  APPLICANT:  Lu, Yifeng
;  TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
;  FILE REFERENCE: 00925
;  CURRENT APPLICATION NUMBER: US/10/408,967
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; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-967-8

  Query Match   99.6%; Score 927; DB 12; Length 373;
  Best Local Similarity   100.0%; Pred. No. 8.8e-87;
  Matches 188; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
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Db        186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 245

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy        182 PGLKRKAE 189
              ||||||||
Db        366 PGLKRKAE 373
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RESULT 15
US-10-060-036-72
; Sequence 72, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-060-036-72

  Query Match   99.6%; Score 927; DB 14; Length 373;
  Best Local Similarity   100.0%; Pred. No. 8.8e-87;
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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
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Db        186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 245

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy        182 PGLKRKAE 189
              ||||||||
Db        366 PGLKRKAE 373
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Search completed: September 29, 2004, 18:48:19
Job time : 21.2878 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:06:43 ; Search time 14.8689 Seconds
(without alignments)
4010.587 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	931	100.0	986	4	Q8IUA4	Q8iua4 homo sapien
2	928	99.7	392	4	Q96B16	Q96b16 homo sapien
3	915	98.3	578	11	Q80W95	Q80w95 mus musculu
4	915	98.3	639	11	Q8K290	Q8k290 mus musculu
5	915	98.3	1046	11	Q8BGK7	Q8bgk7 mus musculu
6	915	98.3	1162	11	Q8BGM9	Q8bgm9 mus musculu
7	912	98.0	375	11	Q8BHF5	Q8bhf5 mus musculu
8	911	97.9	356	11	Q8BH78	Q8bh78 mus musculu
9	904.5	97.2	1163	11	Q8K3G8	Q8k3g8 mus musculu
10	901	96.8	184	6	Q7YRW9	Q7yrw9 bos taurus
11	900.5	96.7	357	11	Q8K3G7	Q8k3g7 mus musculu
12	882	94.7	199	13	Q7T224	Q7t224 gallus gall
13	867	93.1	179	6	Q9GM33	Q9gm33 macaca fasc
14	750	80.6	214	13	Q7T222	Q7t222 carassius a
15	682	73.3	199	4	Q9BQ59	Q9bq59 homo sapien
16	681	73.1	780	11	Q8K4S4	Q8k4s4 mus musculu
17	681	73.1	780	11	Q8K0T0	Q8k0t0 mus musculu
18	672	72.2	760	13	Q90638	Q90638 gallus gall
19	668	71.8	208	13	Q90637	Q90637 gallus gall
20	665	71.4	267	11	Q63765	Q63765 rattus sp.
21	623.5	67.0	236	11	Q8VBU0	Q8vbu0 rattus norv
22	623.5	67.0	237	11	Q8C6D5	Q8c6d5 mus musculu
23	622.5	66.9	643	11	Q8CCU2	Q8ccu2 mus musculu
24	583	62.6	221	13	Q7ZUD6	Q7zud6 brachydanio
25	521	56.0	224	5	Q9VMW1	Q9vmw1 drosophila
26	520	55.9	222	5	Q9VMW4	Q9vmw4 drosophila
27	520	55.9	234	5	Q9VMW3	Q9vmw3 drosophila
28	520	55.9	595	5	Q9VMV9	Q9vmv9 drosophila
29	518	55.6	202	5	Q9VMW2	Q9vmw2 drosophila
30	343	36.8	107	13	Q7T223	Q7t223 carassius a
31	335	36.0	2484	5	Q9U347	Q9u347 caenorhabdi
32	335	36.0	2607	5	Q23187	Q23187 caenorhabdi
33	334	35.9	222	5	Q23188	Q23188 caenorhabdi
34	199.5	21.4	154	5	Q9VIB7	Q9vib7 drosophila
35	199.5	21.4	158	5	Q24199	Q24199 drosophila
36	191	20.5	255	10	O82352	O82352 arabidopsis
37	187	20.1	255	10	Q9SH59	Q9sh59 arabidopsis
38	182	19.5	271	10	Q9SUT9	Q9sut9 arabidopsis
39	165.5	17.8	197	5	Q9NJS2	Q9njs2 leishmania
40	164	17.6	257	10	Q9FFS0	Q9ffs0 arabidopsis
41	163	17.5	275	10	Q9SUR3	Q9sur3 arabidopsis
42	159	17.1	200	10	Q9LT71	Q9lt71 arabidopsis
43	158	17.0	279	10	Q9AWY7	Q9awy7 oryza sativ
44	157	16.9	200	10	Q8LAT8	Q8lat8 arabidopsis
45	154.5	16.6	192	10	Q7XR59	Q7xr59 oryza sativ

ALIGNMENTS

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RESULT 1
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ID   Q8IUA4      PRELIMINARY;      PRT;   986 AA.
AC   Q8IUA4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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DE   RNT4 (RTN4).
GN   RTN4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22376540; PubMed=12488097;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   J. Mol. Biol. 325:299-323(2003).
DR   EMBL; AY102285; AAM64244.1; -.
DR   EMBL; AY123245; AAM64249.1; -.
DR   EMBL; AY123246; AAM64250.1; -.
DR   EMBL; AY123247; AAM64251.1; -.
DR   EMBL; AY123248; AAM64252.1; -.
DR   EMBL; AY123249; AAM64253.1; -.
DR   EMBL; AY123250; AAM64254.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   986 AA;  108449 MW;  0CDE8F647036415A CRC64;

  Query Match           100.0%;  Score 931;  DB 4;  Length 986;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-75;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
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Db        798 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 857

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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Db        858 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 917

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 977
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Qy        181 IPGLKRKAE 189
              |||||||||
Db        978 IPGLKRKAE 986


RESULT 2
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ID   Q96B16      PRELIMINARY;      PRT;   392 AA.
AC   Q96B16;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein (RTN4).
GN   RTN4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22376540; PubMed=12488097;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   J. Mol. Biol. 325:299-323(2003).
DR   EMBL; BC016165; AAH16165.1; -.
DR   EMBL; AY102285; AAM64242.1; -.
DR   EMBL; AY102278; AAM64247.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   392 AA;  42274 MW;  D7B2AA5E839E58AD CRC64;

  Query Match             99.7%;  Score 928;  DB 4;  Length 392;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-75;
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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 263

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 323

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 383

Qy        181 IPGLKRKAE 189
              |||||||||
Db        384 IPGLKRKAE 392


RESULT 3
Q80W95
ID   Q80W95      PRELIMINARY;      PRT;   578 AA.
AC   Q80W95;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-A (Fragment).
GN   NOGO-A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tozaki H., Hirata T.;
RT   "The partial sequence of mouse nogo-A cDNA clone#4109.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB073672; BAC75974.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   578 AA;  63696 MW;  832670C171E4AC61 CRC64;

  Query Match             98.3%;  Score 915;  DB 11;  Length 578;
  Best Local Similarity   98.4%;  Pred. No. 4.2e-74;
  Matches  186;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 449

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        450 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 509

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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                    ||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        510 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 569

Qy        181 IPGLKRKAE 189
                    |||||||||
Db        570 IPGLKRKAE 578


RESULT 4
Q8K290
ID   Q8K290      PRELIMINARY;      PRT;   639 AA.
AC   Q8K290;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032192; AAH32192.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   639 AA;  70312 MW;  309A19DA37603F11 CRC64;

  Query Match             98.3%;  Score 915;  DB 11;  Length 639;
  Best Local Similarity   98.4%;  Pred. No. 4.7e-74;
  Matches  186;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 510

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        511 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 570

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              |||||||||||||||||||||||||:||||||||||||||||||:||||||||||||
Db        571 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 630

Qy        181 IPGLKRKAE 189
              |||||||||
Db        631 IPGLKRKAE 639


RESULT 5
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Q8BGK7
ID   Q8BGK7      PRELIMINARY;      PRT;  1046 AA.
AC   Q8BGK7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102280; AAM73502.1; -.
DR   EMBL; AY102286; AAM73507.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1046 AA;  114221 MW;  8CE2E2238ED51222 CRC64;

  Query Match             98.3%;  Score 915;  DB 11;  Length 1046;
  Best Local Similarity   98.4%;  Pred. No. 8e-74;
  Matches  186;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 917

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        918 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 977

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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                    ||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        978 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1037

Qy        181 IPGLKRKAE 189
                  |||||||||
Db       1038 IPGLKRKAE 1046


RESULT 6
Q8BGM9
ID   Q8BGM9      PRELIMINARY;      PRT;  1162 AA.
AC   Q8BGM9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102284; AAM73506.1; -.
DR   EMBL; AY102286; AAM73511.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1162 AA;  126613 MW;  855697FBEE11781F CRC64;

  Query Match             98.3%;  Score 915;  DB 11;  Length 1162;
  Best Local Similarity   98.4%;  Pred. No. 9e-74;
  Matches  186;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1033

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1093

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              |||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db       1094 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1153

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1154 IPGLKRKAE 1162
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RESULT 7
Q8BHF5
ID   Q8BHF5      PRELIMINARY;      PRT;   375 AA.
AC   Q8BHF5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102282; AAM73504.1; -.
DR   EMBL; AY102286; AAM73509.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
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DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   375 AA;  40300 MW;  23D9EB19BE671AE6 CRC64;

  Query Match             98.0%;  Score 912;  DB 11;  Length 375;
  Best Local Similarity   97.9%;  Pred. No. 4.8e-74;
  Matches  185;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 246

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        247 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 306

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              |||||||||||||||||||||||||:||||||||||||||||||:||||||||||||
Db        307 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 366

Qy        181 IPGLKRKAE 189
              |||||||||
Db        367 IPGLKRKAE 375


RESULT 8
Q8BH78
ID   Q8BH78      PRELIMINARY;      PRT;   356 AA.
AC   Q8BH78;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102281; AAM73503.1; -.
DR   EMBL; AY102286; AAM73508.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   356 AA;  38403 MW;  4366C03BA9630B56 CRC64;

  Query Match             97.9%;  Score 911;  DB 11;  Length 356;
  Best Local Similarity   98.4%;  Pred. No. 5.6e-74;
  Matches  185;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 228

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 288

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||:||||||||||||||||||:||||||||||||
Db        289 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 348

Qy        182 PGLKRKAE 189
              ||||||||
Db        349 PGLKRKAE 356


RESULT 9
Q8K3G8
ID   Q8K3G8      PRELIMINARY;      PRT;  1163 AA.
AC   Q8K3G8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-A.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Long M., Li R., Ju G.;
RT   "Cloning and expression of the mouse Nogo-A protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114152; AAM77068.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
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DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;

  Query Match             97.2%;  Score 904.5;  DB 11;  Length 1163;
  Best Local Similarity   97.9%;  Pred. No. 8e-73;
  Matches  186;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        974 SVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 1033

Qy         60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFA 119
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 1093

Qy        120 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 179
              |||||||||||||||||||||||||||:||||||||||||||||:||||||||||
Db       1094 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQA 1153

Qy        180 KIPGLKRKAE 189
              ||||||||||
Db       1154 KIPGLKRKAE 1163


RESULT 10
Q7YRW9
ID   Q7YRW9      PRELIMINARY;      PRT;   184 AA.
AC   Q7YRW9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4w (Fragment).
GN   RTN4.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164744; AAP47319.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   184 AA;  20671 MW;  DE990E03BBAF84A1 CRC64;

  Query Match             96.8%;  Score 901;  DB 6;  Length 184;
  Best Local Similarity   98.9%;  Pred. No. 2.1e-73;
  Matches  182;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSD 65
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                ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db            1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSD 60

Qy           66 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVF 125
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVF 120

Qy          126 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 185
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180

Qy          186 RKAE 189
                ||||
Db          181 RKAE 184
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RESULT 11
Q8K3G7
ID   Q8K3G7   PRELIMINARY;   PRT;   357 AA.
AC   Q8K3G7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-B.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Li R., Long M., Shen J., Ju G.;
RT   "Cloning and expression of the mouse Nogo-B protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114153; AAM77069.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

  Query Match   96.7%; Score 900.5; DB 11; Length 357;
  Best Local Similarity   97.9%; Pred. No. 5e-73;
  Matches 185; Conservative   2; Mismatches   1; Indels   1; Gaps   1;

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Qy            2 VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
                ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 228

Qy           61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
                |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db          229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 288

Qy          121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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                    ||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        289 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 348

Qy        181 IPGLKRKAE 189
              |||||||||
Db        349 IPGLKRKAE 357


RESULT 12
Q7T224
ID   Q7T224      PRELIMINARY;      PRT;   199 AA.
AC   Q7T224;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4-C.
GN   RTN4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164737; AAP47312.1; -.
SQ   SEQUENCE   199 AA;  22293 MW;  07CF4E4EF2723251 CRC64;

  Query Match             94.7%;  Score 882;  DB 13;  Length 199;
  Best Local Similarity   93.6%;  Pred. No. 1.2e-71;
  Matches  176;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              |||||||||||||||:||:||:|:|||||:  |||:| |:||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESDVAVSEDLIQKYSSVVLGHINGTVKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLVNKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              |||||| |
Db        192 PGLKRKTE 199


RESULT 13
Q9GM33
ID   Q9GM33      PRELIMINARY;      PRT;   179 AA.
AC   Q9GM33;
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DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049853; BAB16739.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   179 AA;  19949 MW;  5F8CD4383FEE9E02 CRC64;

  Query Match             93.1%;  Score 867;  DB 6;  Length 179;
  Best Local Similarity   98.3%;  Pred. No. 2.4e-70;
  Matches  176;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 70
               :|||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db           1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIQAIQKSDEGHPF 60

Qy          71 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGA 130
               ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db          61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLRFAVLMWVFTYVGA 120

Qy         131 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 189
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179


RESULT 14
Q7T222
ID   Q7T222      PRELIMINARY;      PRT;   214 AA.
AC   Q7T222;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4-M.
GN   RTN4.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164754; AAP47329.1; -.
SQ   SEQUENCE   214 AA;  24063 MW;  E9B603B043159DD9 CRC64;

  Query Match             80.6%;  Score 750;  DB 13;  Length 214;
  Best Local Similarity   75.0%;  Pred. No. 1e-59;
  Matches  141;  Conservative   24;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |||||||||:::|||||||| |||||:| ||:|| :|:||||||||||||||||::||:
Db         27 VVDLLYWRDLQRTGVVFGASLLLLLSLSVCSIISVISYVALALLSVTISFRIYKGILQAV 86

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              |||::|||||: ||: :: || ||||||||::|| |:|| ||||||||||:||||||||||
Db         87 QKSEDGHPFKMYLDKDIGISSELVQKYSDTALAHINCVIKELRRLFLVEDLVDSLKFAVF 146

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||: |||||||||||||: ||  || |||||:|||||||| || || :|| | ||||||
Db        147 MWILTYVGALFNGLTLLIMGLIGTFSWPVIYEKHQAQIDHYYGLVNKQIKDVMGKIQAKI 206

Qy        182 PGLKRKAE 189
              || | | |
Db        207 PGAKPKTE 214


RESULT 15
Q9BQ59
ID   Q9BQ59      PRELIMINARY;      PRT;   199 AA.
AC   Q9BQ59;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to reticulon 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003003; AAH03003.1; -.
DR   EMBL; BC000314; AAH00314.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   GO; GO:0000786; C:nucleosome; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
DR   GO; GO:0006334; P:nucleosome assembly; IEA.
DR   InterPro; IPR001951; Histone_H4.
DR   InterPro; IPR003388; Reticulon.
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DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00047; HISTONE_H4; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 73.3%; Score 682; DB 4; Length 199;
Best Local Similarity 68.4%; Pred. No. 1.3e-53;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db         73 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|||||| ||||   ::   :||||||||
Db        133 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 192

Qy        183 GLKRKAE 189
              | || ||
Db        193 GAKRHAE 199
```

Search completed: September 29, 2004, 18:19:48
Job time : 15.8689 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 2.70944 Seconds
(without alignments)
3632.211 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	931	100.0	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
2	911	97.9	199	1	RTN4_MOUSE	Q99p72 mus musculu
3	908	97.5	1163	1	RTN4_RAT	Q9jk11 rattus norv
4	682	73.3	776	1	RTN1_HUMAN	Q16799 homo sapien
5	681	73.1	777	1	RTN1_RAT	Q64548 rattus norv
6	624.5	67.1	236	1	RTN3_HUMAN	O95197 homo sapien
7	623.5	67.0	237	1	RTN3_MOUSE	Q9es97 mus musculu
8	473.5	50.9	545	1	RTN2_HUMAN	O75298 homo sapien
9	473	50.8	471	1	RTN2_MOUSE	O70622 mus musculu
10	93.5	10.0	197	1	AR61_DROME	Q9ves1 drosophila
11	88.5	9.5	1278	1	NPC1_HUMAN	O15118 homo sapien
12	88	9.5	468	1	ACH5_HUMAN	P30532 homo sapien
13	87.5	9.4	296	1	YBZ7_YEAST	P38279 saccharomyc
14	84	9.0	744	1	PRES_RAT	Q9eph0 rattus norv
15	83	8.9	578	1	MDLB_BUCBP	Q89a96 buchnera ap
16	83	8.9	744	1	PRES_MERUN	Q9jkq2 meriones un
17	83	8.9	744	1	PRES_MOUSE	Q99nh7 mus musculu

18	82.5	8.9	570	1	SECD_STRCO	Q53955 streptomyce
19	82	8.8	589	1	Y015_MYCGE	P47261 mycoplasma
20	81.5	8.8	324	1	MRAY_LISIN	Q929y0 listeria in
21	81	8.7	329	1	O5T2_HUMAN	Q8ngg2 homo sapien
22	81	8.7	993	1	NISB_LACLA	P20103 lactococcus
23	80.5	8.6	299	1	Y779_METJA	Q58189 methanococc
24	80.5	8.6	470	1	YMP8_CAEEL	P53993 caenorhabdi
25	80.5	8.6	502	1	OXAA_AQUAE	O66561 aquifex aeo
26	80.5	8.6	839	1	TLR4_PANPA	Q9ttn0 pan paniscu
27	80	8.6	744	1	PRES_HUMAN	P58743 homo sapien
28	79.5	8.5	499	1	UBPG_YEAST	Q02863 saccharomyc
29	79	8.5	312	1	OLF2_CHICK	P37068 gallus gall
30	79	8.5	388	1	YUBA_BACSU	O32086 bacillus su
31	79	8.5	839	1	TLR4_HUMAN	O00206 homo sapien
32	78	8.4	349	1	MRAY_CHLPN	Q9z706 chlamydia p
33	78	8.4	507	1	TLCB_RICPR	Q9zdf2 rickettsia
34	78	8.4	607	1	GLMS_AGRT5	Q8ueh1 a glucosami
35	77.5	8.3	267	1	YTXD_BACME	P46826 bacillus me
36	77.5	8.3	503	1	C72R_ARATH	Q9sae1 arabidopsis
37	77.5	8.3	1277	1	NPC1_PIG	P56941 sus scrofa
38	77	8.3	580	1	MDLB_BUCAI	P57552 buchnera ap
39	76.5	8.2	221	1	YA78_AQUAE	O67171 aquifex aeo
40	76	8.2	284	1	HTPX_METJA	Q59076 methanococc
41	76	8.2	286	1	YL33_ARCFU	O28147 archaeoglob
42	76	8.2	556	1	NU2M_PODAN	P15578 podospora a
43	76	8.2	4351	1	FAT2_RAT	O88277 rattus norv
44	75.5	8.1	307	1	OXA2_LACPL	Q88wr8 lactobacill
45	75.5	8.1	328	1	YM31_ARCFU	O28052 archaeoglob

ALIGNMENTS

```
RESULT 1
RTN4_HUMAN
ID   RTN4_HUMAN     STANDARD;      PRT;  1192 AA.
AC   Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC   Q9Y5U6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE   protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN   RTN4 OR NOGO OR ASY OR KIAA0886.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20129242; PubMed=10667780;
RA   Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA   Michalovich D., Simmons D.L., Walsh F.S.;
RT   "Inhibitor of neurite outgrowth in humans.";
RL   Nature 403:383-384(2000).
RN   [2]
```

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT 2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clone with function of inhibiting cancer cell
RT growth.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN [12]
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
RC TISSUE=Brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RA Sha J.H., Zhou Z.M., Li J.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [14]
RP TOPOLOGY.
RC TISSUE=Brain;
RX MEDLINE=20129259; PubMed=10667797;
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
RT "Identification of the Nogo inhibitor of axon regeneration as a
RT Reticulon protein.";
RL Nature 403:439-444(2000).
RN [15]
RP FUNCTION.
RC TISSUE=Brain;
RX MEDLINE=21069055; PubMed=11201742;
RA Fournier A.E., Grandpre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

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RT   regeneration.";
RL   Nature 409:341-346(2001).
RN   [16]
RP   REVIEW.
RX   MEDLINE=21888956; PubMed=11891768;
RA   Ng C.E.L., Tang B.L.;
RT   "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT   regeneration.";
RL   J. Neurosci. Res. 67:559-565(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults.
CC       Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC       This is likely consecutive to their change in subcellular
CC       location, from the mitochondria to the endoplasmic reticulum,
CC       after binding and sequestration.
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum. Anchored to the membrane of the endoplasmic reticulum
CC       through 2 putative transmembrane domains.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
CC         IsoId=Q9NQC3-1; Sequence=Displayed;
CC       Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
CC         IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC       Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
CC         IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC       Name=4;
CC         IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC   -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC       and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC       widely expressed excepted for the liver. Isoform 3 is expressed in
CC       brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC       specific.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   -!- CAUTION: Ref.11 sequence differs from that shown due to
CC       frameshifts in positions 1149 and 1156.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251383; CAB99248.1; -.
DR   EMBL; AJ251384; CAB99249.1; -.
DR   EMBL; AJ251385; CAB99250.1; -.
DR   EMBL; AB040462; BAB18927.1; -.
DR   EMBL; AB040463; BAB18928.1; -.
DR   EMBL; AF148537; AAG12176.1; -.
DR   EMBL; AF148538; AAG12177.1; -.
DR   EMBL; AF087901; AAG12205.1; -.
DR   EMBL; AF320999; AAG40878.1; -.
DR   EMBL; AF132047; AAD31021.1; -.
DR   EMBL; AF132048; AAD31022.1; -.
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DR   EMBL; AB015639; BAA83712.1; -.
DR   EMBL; AF077050; AAD27783.1; -.
DR   EMBL; AF177332; AAG17976.1; -.
DR   EMBL; AB020693; BAA74909.1; -.
DR   EMBL; BC001035; AAH01035.1; -.
DR   EMBL; BC007109; AAH07109.1; -.
DR   EMBL; BC014366; AAH14366.1; -.

  Query Match             100.0%;  Score 931;  DB 1;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-71;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAE 189
              |||||||||
Db       1184 IPGLKRKAE 1192


RESULT 2
RTN4_MOUSE
ID   RTN4_MOUSE     STANDARD;      PRT;   199 AA.
AC   Q99P72; Q9CTE3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN   RTN4 OR NOGO.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3T3-L1; TISSUE=Adipocyte;
RA   Coulson A.C., Craggs P.D., Morris N.J.;
RT   "Mouse vp20/RTN4C cDNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 170-199 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms may be produced;
CC       Name=1;
CC         IsoId=Q99P72-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF326337; AAK08076.1; -.
DR   EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   DOMAIN        1     25       CYTOPLASMIC (Potential).
FT   TRANSMEM     26     50       POTENTIAL.
FT   DOMAIN       51    137       LUMENAL (Potential).
FT   TRANSMEM    138    162       POTENTIAL.
FT   DOMAIN      163    199       CYTOPLASMIC (Potential).
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FT   DOMAIN       12    199       RETICULON.
SQ   SEQUENCE   199 AA;  22466 MW;  07BE5D580059ED9C CRC64;

  Query Match             97.9%;  Score 911;  DB 1;  Length 199;
  Best Local Similarity   98.4%;  Pred. No. 1.4e-70;
  Matches  185;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              ||||||||||||||||||||||||:||||||||||||||||||:||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 191

Qy        182 PGLKRKAE 189
              ||||||||
Db        192 PGLKRKAE 199


RESULT 3
RTN4_RAT
ID   RTN4_RAT       STANDARD;      PRT;  1163 AA.
AC   Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Glut4 vesicle 20 kDa protein).
GN   RTN4 OR NOGO.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX   MEDLINE=99249816; PubMed=10231557;
RA   Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT   "Cloning and characterization of a 22 kDa protein from rat adipocytes:
RT   a new member of the reticulon family.";
RL   Biochim. Biophys. Acta 1450:68-76(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20129258; PubMed=10667796;
RA   Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA   Spillmann A.A., Christ F., Schwab M.E.;
RT   "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
RT   antigen for monoclonal antibody IN-1.";
RL   Nature 403:434-439(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RC   STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
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RA   Ito T., Schwartz S.M.;
RT   "Cloning of a member of the reticulon gene family in rat: one of two
RT   minor splice variants.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   MEDLINE=22033691; PubMed=12037567;
RA   GrandPre T., Li S., Strittmatter S.M.;
RT   "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL   Nature 417:547-551(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=Nogo-A, NI-220-250;
CC         IsoId=Q9JK11-1; Sequence=Displayed;
CC       Name=2; Synonyms=Nogo-B, Foocen-M1;
CC         IsoId=Q9JK11-2; Sequence=VSP_005658;
CC       Name=3; Synonyms=Nogo-C, VP20;
CC         IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
CC       Name=4; Synonyms=Foocen-M2;
CC         IsoId=Q9JK11-4; Sequence=VSP_005659;
CC   -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC       nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC       present in dorsal root ganglion, sciatic nerve and PC12 cells
CC       after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC       cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC       level in skeletal muscle. In adult animals isoform 1 is expressed
CC       mainly in the nervous system.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF051335; AAF01564.1; -.
DR   EMBL; AJ242961; CAB71027.1; -.
DR   EMBL; AJ242962; CAB71028.1; -.
DR   EMBL; AJ242963; CAB71029.1; -.
DR   EMBL; AF132045; AAD31019.1; -.
DR   EMBL; AF132046; AAD31020.1; -.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   InterPro; IPR003388; Reticulon.
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DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   DOMAIN        1    989       CYTOPLASMIC (Potential).
FT   TRANSMEM    990   1010       POTENTIAL.
FT   DOMAIN      1011   1104       LUMENAL (Potential).
FT   TRANSMEM    1105   1125       POTENTIAL.
FT   DOMAIN      1126   1163       CYTOPLASMIC (Potential).
FT   DOMAIN       976   1163       RETICULON.
FT   DOMAIN        33     46       POLY-GLU.
FT   DOMAIN        73     76       POLY-ALA.
FT   DOMAIN       140    145       POLY-PRO.
FT   VARSPLIC       1    964       Missing (in isoform 3).
FT                                 /FTId=VSP_005656.
FT   VARSPLIC     965    975       AVLSAELSKTS -> MDGQKKHWKDK (in isoform
FT                                 3).
FT                                 /FTId=VSP_005657.
FT   VARSPLIC     173    975       Missing (in isoform 2).
FT                                 /FTId=VSP_005658.
FT   VARSPLIC     192    975       Missing (in isoform 4).
FT                                 /FTId=VSP_005659.
FT   CONFLICT    1130   1131       MISSING (IN REF. 3; AAD31020).
SQ   SEQUENCE    1163 AA;  126386 MW;  8CB894B09E94F0B6 CRC64;

  Query Match             97.5%;  Score 908;  DB 1;  Length 1163;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-69;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
              ||||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy        181 IPGLKRKAE 189
              |||||||||:
Db       1155 IPGLKRKAD 1163


RESULT 4
RTN1_HUMAN
ID   RTN1_HUMAN     STANDARD;      PRT;   776 AA.
AC   Q16799; Q16800; Q16801;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon 1 (Neuroendocrine-specific protein).
GN   RTN1 OR NSP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=93293865; PubMed=7685762;
RA   Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
RA   Ramaekers F.C.S., Van de Ven W.J.M.;
RT   "Cloning and expression of alternative transcripts of a novel
RT   neuroendocrine-specific gene and identification of its 135-kDa
RT   translational product.";
RL   J. Biol. Chem. 268:13439-13447(1993).
RN   [2]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=96429995; PubMed=8833145;
RA   Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA   Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT   "Genomic organization of the human NSP gene, prototype of a novel gene
RT   family encoding reticulons.";
RL   Genomics 32:191-199(1996).
RN   [3]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=98228245; PubMed=9560466;
RA   Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA   Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;
RT   "Neuronal differentiation is accompanied by NSP-C expression.";
RL   Cell Tissue Res. 292:229-237(1998).
CC   -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC       membrane trafficking in neuroendocrine cells.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=RTN1-A; Synonyms=NSP-A;
CC         IsoId=Q16799-1; Sequence=Displayed;
CC       Name=RTN1-B; Synonyms=NSP-B;
CC         IsoId=Q16799-2; Sequence=VSP_005644;
CC       Name=RTN1-C; Synonyms=NSP-C;
CC         IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC       AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC       IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC   -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; L10333; AAA59950.1; -.
DR   EMBL; L10334; AAA59951.1; -.
DR   EMBL; L10335; AAA59952.1; -.
DR   PIR; A46583; A46583.
DR   PIR; I60904; I60904.
DR   Genew; HGNC:10467; RTN1.
```

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DR   MIM; 600865; -.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0030182; P:neuron differentiation; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW   Phosphorylation.
FT   TRANSMEM    603    623       POTENTIAL.
FT   TRANSMEM    726    746       POTENTIAL.
FT   DOMAIN      589    776       RETICULON.
FT   DOMAIN      609    612       POLY-LEU.
FT   VARSPLIC      1    420       Missing (in isoform RTN1-B).
FT                                /FTId=VSP_005644.
FT   VARSPLIC      1    568       Missing (in isoform RTN1-C).
FT                                /FTId=VSP_005645.
FT   VARSPLIC    569    588       GPGPLGPGAPPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT                                KSQ (in isoform RTN1-C).
FT                                /FTId=VSP_005646.
SQ   SEQUENCE   776 AA;  83617 MW;  CA5B6232353096FE CRC64;

  Query Match             73.3%;  Score 682;  DB 1;  Length 776;
  Best Local Similarity   68.4%;  Pred. No. 1.7e-50;
  Matches  128;  Conservative   31;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :||||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        590 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:||||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||||
Db        650 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|||||| ||||   ::   :||||||||
Db        710 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy        183 GLKRKAE 189
              | || ||
Db        770 GAKRHAE 776


RESULT 5
RTN1_RAT
ID   RTN1_RAT       STANDARD;      PRT;   777 AA.
AC   Q64548; Q64547;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN   RTN1 OR NSP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
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RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC   STRAIN=Wistar; TISSUE=Brain cortex;
RX   MEDLINE=96386034; PubMed=8793864;
RA   Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA   Georgiev G.P., Buchman V.L.;
RT   "Intracellular compartmentalization of two differentially spliced s-
RT   rex/NSP mRNAs in neurons.";
RL   Mol. Cell. Neurosci. 7:289-303(1996).
CC   -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC       membrane trafficking in neuroendocrine cells.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=RTN1-B; Synonyms=S-RexB;
CC         IsoId=Q64548-1; Sequence=Displayed;
CC       Name=RTN1-S; Synonyms=S-RexS;
CC         IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC       PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC       HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC       EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC       TYPES.
CC   -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC       HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC       DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC       THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC       DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC       HINDBRAIN.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U17604; AAC53046.1; -.
DR   EMBL; U17603; AAC53045.1; -.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   TRANSMEM    604    624       POTENTIAL.
FT   TRANSMEM    727    747       POTENTIAL.
FT   DOMAIN      590    777       RETICULON.
FT   DOMAIN      610    613       POLY-LEU.
FT   VARSPLIC      1    569       Missing (in isoform RTN1-S).
FT                                /FTId=VSP_005647.
FT   VARSPLIC    570    589       IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT                                KSQ (in isoform RTN1-S).
FT                                /FTId=VSP_005648.
SQ   SEQUENCE   777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;
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  Query Match             73.1%;  Score 681;  DB 1;  Length 777;
  Best Local Similarity   67.9%;  Pred. No. 2.1e-50;
  Matches  127;  Conservative   32;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        591 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 650

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
              |:||||||:|||| |: :|:| :|||::    :|| |:|||||||| ||||||||||
Db        651 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 710

Qy        123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :||||:| ||||   ::   :||||||||
Db        711 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIP 770

Qy        183 GLKRKAE 189
              | || ||
Db        771 GAKRHAE 777


RESULT 6
RTN3_HUMAN
ID   RTN3_HUMAN     STANDARD;      PRT;   236 AA.
AC   O95197;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
DE   protein II) (NSPLII).
GN   RTN3 OR NSPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Retina;
RX   MEDLINE=99265974; PubMed=10331947;
RA   Moreira E.F., Jaworski C.J., Rodriguez I.R.;
RT   "Cloning of a novel member of the reticulon gene family (RTN3): gene
RT   structure and chromosomal localization to 11q13.";
RL   Genomics 58:73-81(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
RT   "Cloning and expression analysis of a cDNA encoding a novel
RT   neuroendocrine-specific protein-like protein 1: NSPL1.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Eye, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
CC       BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
CC       RETINA.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF059524; AAC99319.1; -.
DR   EMBL; AF059529; AAD20951.1; -.
DR   EMBL; AF059525; AAD20951.1; JOINED.
DR   EMBL; AF059526; AAD20951.1; JOINED.
DR   EMBL; AF059527; AAD20951.1; JOINED.
DR   EMBL; AF059528; AAD20951.1; JOINED.
DR   EMBL; AF119297; AAD26810.1; -.
DR   EMBL; BC000634; AAH00634.1; -.
DR   EMBL; BC010556; AAH10556.1; -.
DR   EMBL; BC011394; AAH11394.1; -.
DR   EMBL; BC022993; AAH22993.1; -.
DR   Genew; HGNC:10469; RTN3.
DR   MIM; 604249; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Transmembrane; Endoplasmic reticulum.
FT   TRANSMEM     68     88       POTENTIAL.
FT   TRANSMEM    177    197       POTENTIAL.
FT   DOMAIN       48    236       RETICULON.
SQ   SEQUENCE   236 AA;  25609 MW;  DDC6A4544ABCDFB7 CRC64;

  Query Match             67.1%;  Score 624.5;  DB 1;  Length 236;
  Best Local Similarity   60.5%;  Pred. No. 3.9e-46;
  Matches  115;  Conservative   39;  Mismatches   35;  Indels    1;  Gaps    1;
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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :| ||::|||:|||| ||| :| :|||| ||::|| :|: |||||||||||||| ||||
Db         47 AVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 106

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              :|||:|||||:|||: :: :| |    | |:|: |:|  :| : |||||:||||||| ||
Db        107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
               ||: |||||:|||:|||||| : :||||::||::: |||||:|:|    |  : |||||
Db        167 FMWLMTYVGAVFNGITLLILAELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 226

Qy        181 IPGL-KRKAE 189
              :||: |:|||
Db        227 LPGIAKKKAE 236
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RESULT 7
RTN3_MOUSE
ID   RTN3_MOUSE   STANDARD;   PRT;   237 AA.
AC   Q9ES97;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Reticulon protein 3.
GN   RTN3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
RT   "Cloning and expression profile of a novel mouse cDNA encoding a human
RT   RTN3 homolog.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

```
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF195940; AAG31360.1; -.
DR   EMBL; BC014697; AAH14697.1; -.
DR   MGD; MGI:1339970; Rtn3.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Transmembrane; Endoplasmic reticulum.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    167    187       POTENTIAL.
FT   DOMAIN       49    237       RETICULON.
SQ   SEQUENCE   237 AA;  25428 MW;  EB60A0A7AC45F0DE CRC64;

  Query Match             67.0%;  Score 623.5;  DB 1;  Length 237;
  Best Local Similarity   60.5%;  Pred. No. 4.7e-46;
  Matches  115;  Conservative   39;  Mismatches   35;  Indels    1;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :| ||::|||:|||| ||| :| :|||| ||::|| :|: |||||||||||:|| ||||
Db         48 AVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSVIQA 107

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
              :|||:|||||:|||: :: :| |    | |:|: |||  :| : |||||:||||||| ||
Db        108 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDSLKLAV 167

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
               ||: |||||:|||:|||||| : :|||||::||::: |||||:|:|    | : |||||
Db        168 FMWLMTYVGAVFNGITLLILAELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 227

Qy        181 IPGL-KRKAE 189
              :||: |:|||
Db        228 LPGIAKKKAE 237


RESULT 8
RTN2_HUMAN
ID   RTN2_HUMAN     STANDARD;      PRT;   545 AA.
AC   O75298; O60509;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
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DE   protein 1) (NSPLI).
GN   RTN2 OR NSPL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=98360096; PubMed=9693037;
RA   Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
RT   "cDNA cloning, genomic organization, and expression of the human RTN2
RT   gene, a member of a gene family encoding reticulons.";
RL   Genomics 51:98-106(1998).
RN   [2]
RP   SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
RC   TISSUE=Brain;
RX   MEDLINE=98191726; PubMed=9530622;
RA   Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT   "Molecular cloning of a novel mouse gene with predominant muscle and
RT   neural expression.";
RL   Mamm. Genome 9:274-282(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=RTN2-A;
CC         IsoId=O75298-1; Sequence=Displayed;
CC         Note=Isoform RTN2-C is produced by alternative initiation at
CC         Met-341 of isoform RTN2-A;
CC       Name=RTN2-B;
CC         IsoId=O75298-2; Sequence=VSP_005649;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
CC         by alternative initiation at Met-1 and Met-341;
CC   -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
CC       MUSCLE.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; AF004222; AAC32542.1; -.
DR   EMBL; AF004223; AAC32543.1; -.
DR   EMBL; AF004224; AAC32544.1; -.
DR   EMBL; AF038540; AAC14910.1; -.
DR   Genew; HGNC:10468; RTN2.
DR   MIM; 603183; -.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003388; Reticulon.
```

```
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW   Alternative initiation.
FT   CHAIN         1    545       RETICULON PROTEIN 2, ISOFORM RTN2-A.
FT   CHAIN       341    545       RETICULON PROTEIN 2, ISOFORM RTN2-C.
FT   INIT_MET    341    341       FOR ISOFORM RTN2-C.
FT   TRANSMEM    368    388       POTENTIAL.
FT   TRANSMEM    463    483       POTENTIAL.
FT   DOMAIN      345    545       RETICULON.
FT   VARSPLIC    272    344       Missing (in isoform RTN2-B).
FT                                /FTId=VSP_005649.
SQ   SEQUENCE   545 AA;  59263 MW;  971FD2F909E1E9E6 CRC64;

  Query Match             50.9%;  Score 473.5;  DB 1;  Length 545;
  Best Local Similarity   47.3%;  Pred. No. 6.3e-33;
  Matches   95;  Conservative   37;  Mismatches   56;  Indels   13;  Gaps    1;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              | |||||:| : :||||   :  || |  |||||| |::|| ||  ||| |:|: |:||:
Db        345 VADLLYWKDTRTSGVVFTGLMVSLLCLLHFSIVSVAAHLALLLLCGTISLRVYRKVLQAV 404

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
               : |  :||:|||: :: :: |  :: |:     |     :||  |||:|||||| |:|
Db        405 HRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALL 464

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
               :: |:|||:|||||||| :| ||::|::| :|||||| |:||    :    |||:|||
Db        465 FYILTFVGAIFNGLTLLILGVIGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 524

Qy        182 PGL-------------KRKAE 189
              ||              | |||
Db        525 PGTGALASAAAAVSGSKAKAE 545


RESULT 9
RTN2_MOUSE
ID   RTN2_MOUSE     STANDARD;      PRT;   471 AA.
AC   O70622; O70620;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
DE   protein 1) (NSPLI).
GN   RTN2 OR NSPL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC   STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
RX   MEDLINE=98191726; PubMed=9530622;
RA   Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT   "Molecular cloning of a novel mouse gene with predominant muscle and
RT   neural expression.";
RL   Mamm. Genome 9:274-282(1998).
```

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RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC       (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Brain;
CC         IsoId=O70622-1; Sequence=Displayed;
CC       Name=2; Synonyms=Muscle;
CC         IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
CC   -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
CC       tissues.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF038537; AAC14906.1; -.
DR   EMBL; AF038537; AAC14907.1; -.
DR   EMBL; AF038538; AAC14908.1; -.
DR   EMBL; AF038539; AAC14909.1; -.
DR   EMBL; AF093624; AAD13195.1; -.
DR   EMBL; BC031370; AAH31370.1; -.
DR   MGD; MGI:107612; Rtn2.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   TRANSMEM     295     315       POTENTIAL.
FT   DOMAIN       272     471       RETICULON.
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FT   VARSPLIC      1    267       Missing (in isoform 2).
FT                                /FTId=VSP_005650.
FT   VARSPLIC    268    271       PLLL -> MGSK (in isoform 2).
FT                                /FTId=VSP_005651.
SQ   SEQUENCE   471 AA;  51346 MW;  9BBD8F372CF63AD3 CRC64;

  Query Match             50.8%;  Score 473;  DB 1;  Length 471;
  Best Local Similarity   47.0%;  Pred. No. 6e-33;
  Matches   94;  Conservative   38;  Mismatches   56;  Indels   12;  Gaps    1;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              | |||||:| : :| ||   :  || |  |||||| |::||  |  ||| |:|: |:||:
Db        272 VADLLYWKDTRTSGAVFTGLMASLLCLLHFSIVSVAAHLALLGLCATISLRVYRKVLQAV 331

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
               : |  :||:|||: :: :: |  :: |     ||  |  :||  |||:|||||| |:|
Db        332 HRGDGTNPFQAYLDMDLTLTREQTERLSQQIASHVVSTATQLRHFFLVEDLVDSLKLALL 391

Qy        122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
              :: |:|||:|||||:|| :::||:||::| :|||||| |:||    :    |||:|||
Db        392 FYILTFVGAIFNGLTLVILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 451

Qy        182 PGL----------KRKAE 189
              ||             | |||
Db        452 PGTGTLAPTASVSGSKAKAE 471


RESULT 10
AR61_DROME
ID   AR61_DROME     STANDARD;      PRT;   197 AA.
AC   Q9VES1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   ARL-6 interacting protein-1 homolog.
GN   CG10326.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the ARL6ip family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE003714; AAF55348.1; -.
DR   FlyBase; FBgn0038453; CG10326.
KW   Transmembrane.
FT   TRANSMEM     43     63       POTENTIAL.
FT   TRANSMEM     64     84       POTENTIAL.
FT   TRANSMEM    129    149       POTENTIAL.
FT   TRANSMEM    150    170       POTENTIAL.
SQ   SEQUENCE   197 AA;  22233 MW;  7D35ABAD18CE272E CRC64;

  Query Match             10.0%;  Score 93.5;  DB 1;  Length 197;
  Best Local Similarity   23.9%;  Pred. No. 0.45;
  Matches   47;  Conservative   25;  Mismatches   82;  Indels   43;  Gaps    7;

Qy          5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR-------IYKGV 57
              :| |      |||||    | | |    :  :|    | ::|: :::        |: ||
Db         32 VLTWEKQYYAGVVFGVISCLYLVLWYLDLSLITLLSLLGVISILLNYAFPMVSRLIFGGV 91

Qy         58 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLK 117
                    |:   |        |:   ||  |             | :    |  :| ||
Db         92 ---NWDGDQEAKFEDVCGQVCAVKGSLVVWY--------EYLFNERKSTVFV--IVMSLG 138
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Qy        118 FAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK- 176
                  : |    :||: | | |: || : :   |              || ||:;  |: :
Db        139 LLAMAW----IGAIINNLLLMYLATLLILMWP--------------GLQNKDIFKAITQR 180

Qy        177 ----IQAKIPGLKRKAE 189
                    |  ||   ||| :
Db        181 ASKIINEKIQCGKRKLQ 197
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RESULT 11
NPC1_HUMAN
ID   NPC1_HUMAN   STANDARD;   PRT; 1278 AA.
AC   O15118; Q9P130;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Niemann-Pick C1 protein precursor.
GN   NPC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANTS NPC1.
RX   MEDLINE=97362323; PubMed=9211849;
RA   Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,
RA   Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B.,
RA   Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A.,
RA   Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,
RA   Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,
RA   Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,
RA   Markie D., O'Neill R.R., van Diggelen O.P., Elleder M.,
RA   Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;
RT   "Niemann-Pick C1 disease gene: homology to mediators of cholesterol
RT   homeostasis.";
RL   Science 277:228-231(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS.
RX   MEDLINE=99355599; PubMed=10425213;
RA   Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
RA   Carstea E.D.;
RT   "The genomic organization and polymorphism analysis of the human
RT   Niemann-Pick C1 gene.";
RL   Biochem. Biophys. Res. Commun. 261:493-498(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21623216; PubMed=11754101;
RA   Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
RA   Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
RT   "NPC1: Complete genomic sequence, mutation analysis, and
RT   characterization of haplotypes.";
RL   Hum. Mutat. 19:30-38(2002).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=99128318; PubMed=9927649;
RA   Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,

RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III;
RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and
RT lysosomal targeting in cholesterol mobilization.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
RN [5]
RP VARIANT NPD TRP-992.
RX MEDLINE=98299797; PubMed=9634529;
RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,
RA Byers D.M., Dobson M.J., Neumann P.E.;
RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a
RT G3097-->T transversion in NPC1.";
RL Am. J. Hum. Genet. 63:52-54(1998).
RN [6]
RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007;
RP THR-1061 AND VAL-1213.
RX MEDLINE=99452586; PubMed=10521290;
RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,
RA Neumann P.E.;
RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
RT domain.";
RL Am. J. Hum. Genet. 65:1252-1260(1999).
RN [7]
RP VARIANT NPC1 THR-1061.
RX MEDLINE=99452593; PubMed=10521297;
RA Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A.,
RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;
RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant
RT allele in patients of Western European descent and correlates with a
RT classic juvenile phenotype.";
RL Am. J. Hum. Genet. 65:1321-1329(1999).
RN [8]
RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.
RX MEDLINE=99408226; PubMed=10480349;
RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,
RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,
RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,
RA Ohno K.;
RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease
RT type C.";
RL Hum. Genet. 105:10-16(1999).
RN [9]
RP VARIANTS NPC1 GLN-958 AND ALA-1007.
RX MEDLINE=21313111; PubMed=11349231;
RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,
RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;
RT "Niemann-Pick C variant detection by altered sphingolipid trafficking
RT and correlation with mutations within a specific domain of NPC1.";
RL Am. J. Hum. Genet. 68:1361-1372(2001).
RN [10]
RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.
RX MEDLINE=21313105; PubMed=11333381;
RA Millat G., Marcais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,
RA Wenger D.A., Ohno K., Vanier M.T.;
RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels
RT of NPC1 protein, and phenotypes emphasize the functional significance
RT of the putative sterol-sensing domain and of the cysteine-rich
RT luminal loop.";

```
RL   Am. J. Hum. Genet. 68:1373-1385(2001).
RN   [11]
RP   VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.
RX   MEDLINE=21372069; PubMed=11479732;
RA   Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T.,
RA   Millat G.;
RT   "Niemann-Pick type C disease: NPC1 mutations associated with severe
RT   and mild cellular cholesterol trafficking alterations.";
RL   Hum. Genet. 109:24-32(2001).
CC   -!- FUNCTION: Involved in the intracellular trafficking of
CC       cholesterol. May play a role in vesicular trafficking in glia, a
CC       process that may be crucial for maintaining the structural and
CC       functional integrity of nerve terminals.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late
CC       endosomes and lysosomes.
CC   -!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain
CC       containing a di-leucine motif necessary for lysosomal targeting
CC       are critical for mobilization of cholesterol from lysosomes.
CC   -!- PTM: Glycosylated.
CC   -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
CC       type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid
CC       storage disorder, which affects particularly the brain, liver and
CC       spleen, and which is characterized by lysosomal accumulation of
CC       low density lipoprotein derived cholesterol. Clinical features
CC       include variable hepatosplenomegaly and severe progressive
CC       neurological dysfunction such as ataxia, dystonia and dementia.
CC       The age of onset can vary from infancy to late adulthood.
CC   -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
CC       type D (NPD) [MIM:257250]; also known as Niemann-Pick disease
CC       without sphingomyelinase deficiency, or Nova Scotian type. Because
CC       of evidence from biochemical changes, lack of complementation, and
CC       linkage mapping to the same chromosome site, NPD and NPC1 are
CC       considered to be allelic disorders.
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF002020; AAB63982.1; -.
DR   EMBL; AF157379; AAD48006.1; -.
DR   EMBL; AF157365; AAD48006.1; JOINED.
DR   EMBL; AF157366; AAD48006.1; JOINED.
DR   EMBL; AF157367; AAD48006.1; JOINED.
DR   EMBL; AF157368; AAD48006.1; JOINED.
DR   EMBL; AF157369; AAD48006.1; JOINED.
DR   EMBL; AF157370; AAD48006.1; JOINED.
DR   EMBL; AF157371; AAD48006.1; JOINED.
DR   EMBL; AF157372; AAD48006.1; JOINED.
DR   EMBL; AF157373; AAD48006.1; JOINED.
DR   EMBL; AF157374; AAD48006.1; JOINED.
DR   EMBL; AF157375; AAD48006.1; JOINED.
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DR   EMBL; AF157376; AAD48006.1; JOINED.
DR   EMBL; AF157377; AAD48006.1; JOINED.
DR   EMBL; AF157378; AAD48006.1; JOINED.
DR   EMBL; AF338230; AAK25791.1; -.
DR   EMBL; AF123046; AAF28875.1; -.
DR   EMBL; AF123045; AAF28875.1; JOINED.
DR   Genew; HGNC:7897; NPC1.
DR   MIM; 607623; -.
DR   MIM; 257220; -.
DR   MIM; 257250; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005764; C:lysosome; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0005478; F:intracellular transporter activity; TAS.
DR   GO; GO:0015248; F:sterol transporter activity; TAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   InterPro; IPR004765; NP_C_type.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00917; 2A060601; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;
KW   Disease mutation.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23   1278       NIEMANN-PICK C1 PROTEIN.
FT   TRANSMEM    270    290       POTENTIAL.
FT   TRANSMEM    351    371       POTENTIAL.
FT   TRANSMEM    622    642       POTENTIAL.
FT   TRANSMEM    655    675       POTENTIAL.
FT   TRANSMEM    678    698       POTENTIAL.
FT   TRANSMEM    760    780       POTENTIAL.
FT   TRANSMEM    833    853       POTENTIAL.
FT   TRANSMEM   1099   1119       POTENTIAL.
FT   TRANSMEM   1125   1145       POTENTIAL.
FT   TRANSMEM   1196   1216       POTENTIAL.
FT   TRANSMEM   1228   1248       POTENTIAL.
FT   DOMAIN      249    259       POLY-PRO.
FT   DOMAIN      620    785       SSD.
FT   SITE       1275   1278       DI-LEUCINE MOTIF.
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).

  Query Match              9.5%;  Score 88.5;  DB 1;  Length 1278;
  Best Local Similarity   25.7%;  Pred. No. 8.1;
  Matches   39;  Conservative   25;  Mismatches   51;  Indels   37;  Gaps    7;

Qy         46 SVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 105
              ::||||   : :   : :  :   |       | ||  ::  | : ||||    ||  ||
Db        598 NLTISFTAERSIEDELNRESDSDVF------TVVISYAIMFLYISLALGH----IKSCRR 647

Qy        106 LFLVDD---------LVDSLKFAVLMWVFTYVGALFNGLTLLILALI----------SLF 146
              | |||          |:     |  : ||:|:|     |||::: :|          ::|
Db        648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy        147 SVPVIYERHQ----AQIDHYLGLANKNVKDAM 174
               :   |:| :      :|  ||     |  :|
Db        704 ILVQAYQRDERLQGETLDQQLGRVLGEVAPSM 735
```

RESULT 12
ACH5_HUMAN
ID   ACH5_HUMAN   STANDARD;   PRT;   468 AA.
AC   P30532; Q15824; Q99554;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neuronal acetylcholine receptor protein, alpha-5 chain precursor.
GN   CHRNA5 OR NACHRA5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92179225; PubMed=1542648;
RA   Chini B., Clementi F., Hukovic N., Sher E.;
RT   "Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic
RT   receptor subunit gene are expressed in neuronal and nonneuronal human
RT   cell lines.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1572-1576(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97062879; PubMed=8906617;
RA   Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA   Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT   "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT   2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT   expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT   beta 4 subunits.";
RL   J. Mol. Neurosci. 7:217-228(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97162233; PubMed=9009220;
RA   Groot Kormelink P.J., Luyten W.H.M.L.;
RT   "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT   nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT   expression of seven nAChR subunits in the human neuroblastoma cell
RT   line SH-SY5Y and/or IMR-32.";
RL   FEBS Lett. 400:309-314(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,
RA   Tenchini M.L.;
RT   "Characterization of the genomic structure of human nicotinic
RT   acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of
RT   two novel introns in the 3' untranslated region of CHRNA3 and of a
RT   tail-to-tail overlap between CHRNA3 and CHRNA5.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different type
CC of subunits: alpha and non-alpha (betA).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC ---

CC ---
DR EMBL; M83712; AAA58357.1; -.
DR EMBL; U62434; AAB40112.1; -.
DR EMBL; Y08419; CAA69696.1; -.
DR EMBL; AJ306481; CAC34820.1; -.
DR EMBL; AJ306482; CAC34820.1; JOINED.
DR EMBL; AJ306483; CAC34820.1; JOINED.
DR EMBL; AJ306484; CAC34820.1; JOINED.
DR EMBL; AJ306485; CAC34820.1; JOINED.
DR EMBL; AJ306486; CAC34820.1; JOINED.
DR EMBL; BC033639; AAH33639.1; -.
DR PIR; A38223; A38223.
DR Genew; HGNC:1959; CHRNA5.
DR MIM; 118505; -.
DR InterPro; IPR006029; Neu_channel_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

```
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    468       NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT                                 ALPHA-5 CHAIN.
FT   DOMAIN       23    249       EXTRACELLULAR.
FT   TRANSMEM    250    274       POTENTIAL.
FT   TRANSMEM    282    299       POTENTIAL.
FT   TRANSMEM    316    337       POTENTIAL.
FT   DOMAIN      338    429       CYTOPLASMIC.
FT   TRANSMEM    430    448       POTENTIAL.
FT   DISULFID    170    184       BY SIMILARITY.
FT   DISULFID    234    235       ASSOCIATED WITH RECEPTOR ACTIVATION
FT                                 (BY SIMILARITY).
FT   CARBOHYD    155    155       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    229    229       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     23     34       RCGLAGAAGGAQ -> ALRSSRARRAAR (IN REF. 1).
FT   CONFLICT    128    128       V -> S (IN REF. 1).
FT   CONFLICT    365    365       C -> S (IN REF. 1).
FT   CONFLICT    398    398       D -> N (IN REF. 2 AND 4).
FT   CONFLICT    405    405       R -> T (IN REF. 1).
SQ   SEQUENCE   468 AA;  53054 MW;  7FE91A2E362289C0 CRC64;

  Query Match              9.5%;  Score 88;  DB 1;  Length 468;
  Best Local Similarity   20.9%;  Pred. No. 3.2;
  Matches   40;  Conservative   29;  Mismatches   66;  Indels   56;  Gaps    5;

Qy         24 LLLSLTVFSIV----------SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 70
              :|:|||||| :|              :  |:   :: ||:|  :    |    :|   |
Db        288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHHRSSSTHNA 347

Qy         71 RAYL-------------------------ESEVAISEELVQKYSNSALGHVNCTIKEL 103
               | |                          |:|     :  :    :||  :    : :
Db        348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALDSIRYITRHI 407

Qy        104 RRLFLVDDLVDSLKF------AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 157
              :   | ::|:  ||       : :| | :|          |:  : || |||||:
Db        408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS---------IVGSLGLF-VPVIYKWANI 457

Qy        158 QIDHYLGLANK 168
               |  ::| |||
Db        458 LIPVHIGNANK 468


RESULT 13
YBZ7_YEAST
ID   YBZ7_YEAST     STANDARD;      PRT;   296 AA.
AC   P38279;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Hypothetical 33.5 kDa protein in MRPS9-YSW1 intergenic region.
GN   YBR147W OR YBR1124.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RA   Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
RA   Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
RA   Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,
RA   Gruenbein R., Hedges D., Kiesau P., Korol S., Krems B., Proft M.,
RA   Siegers K., Baur A., Boles E., Miosga T.,
RA   Schaaff-Gerstenschlaeger I., Zimmermann F.K.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z36016; CAA85105.1; -.
DR   PIR; S46018; S46018.
DR   GermOnline; 138690; -.
DR   SGD; S0000351; YBR147W.
DR   InterPro; IPR006603; CTNS.
DR   Pfam; PF04193; PQ-loop; 2.
DR   SMART; SM00679; CTNS; 2.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     13     33       POTENTIAL.
FT   TRANSMEM     45     65       POTENTIAL.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    164    184       POTENTIAL.
FT   TRANSMEM    200    220       POTENTIAL.
FT   TRANSMEM    239    259       POTENTIAL.
FT   TRANSMEM    263    283       POTENTIAL.
SQ   SEQUENCE   296 AA;  33496 MW;  50D65896A1BAFB43 CRC64;

  Query Match              9.4%;  Score 87.5;  DB 1;  Length 296;
  Best Local Similarity   27.4%;  Pred. No. 2.2;
  Matches   54;  Conservative   25;  Mismatches   71;  Indels   47;  Gaps   11;

Qy         17 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY----KGVIQAIQKS-DEGH--- 68
              | || :  ||     ::: : ||  || | : |    |    | ::| ::|: |  |
Db         61 VMGAMMQNLLP----TMIILAAYYTLADLILLIQCMWYDKEKKSILQEVKKNVDPVHLPP 116

Qy         69 -----------PFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDS-- 115
                         |  |      | ||  | ||:  ||     :|| |  |  | |: |
Db        117 ANPINETVLQDVFNEYEPLLPRIEEEDSQSYSSLELGR-TIVVKE-RENFFNDFLIVSGV 174

Qy        116 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA 175
              |   :| |  :|   | ||:     |  : ::|       |||  ||         |:
Db        175 LIAGILSWYISYCSGLDNGIPKKKPAFEQI-NLP-------AQILGYL--------SAIL 218

Qy        176 KIQAKIP----GLKRKA 188
               : ::||      |||:
Db        219 YLGSRIPQIVLNFKRKS 235
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RESULT 14
PRES_RAT
ID   PRES_RAT       STANDARD;      PRT;   744 AA.
AC   Q9EPH0; Q9ERC6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Prestin.
GN   SLC26A5 OR PRES.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND TOPOLOGY.
RC   TISSUE=Cochlea;
RX   MEDLINE=21173705; PubMed=11274441;
RA   Ludwig J., Oliver D., Frank G., Kloecker N., Gummer A.W., Fakler B.;
RT   "Reciprocal electromechanical properties of rat prestin: The motor
RT   molecule of rat outer hair cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4178-4183(2001).
RN   [2]
RP   SEQUENCE OF 249-668 FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Beisel K.W., Nelson N.C., Beisel C.L., Delimont D.C., He D.Z.Z.,
RA   Fritzsch B.;
RT   "Dynamic developmental expression of cochlear hair cell genes: prestin
RT   and otoferlin.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1-20 FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Weber T., Zimmermann U., Winter H., Mack A., Koepschall I.,
RA   Rohbock K., Zenner H.P., Knipper M.;
RT   "Thyroid horomone is a critical determinant for the regulation of the
RT   cochlear motor protein prestin.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=20574880; PubMed=11125015;
RA   Belyantseva I.A., Adler H.J., Curi R., Frolenkov G.I., Kachar B.;
RT   "Expression and localization of prestin and the sugar transporter
RT   GLUT-5 during development of electromotility in cochlear outer hair
RT   cells.";
RL   J. Neurosci. 20:RC116-RC116(2000).
RN   [5]
RP   MODE OF ACTION, AND MUTAGENESIS OF ASP-154; ASP-155; GLU-169; LYS-177;
RP   ARG-197; LYS-233; LYS-235; ARG-236; GLU-277; ARG-281; LYS-283;
RP   LYS-285; ASP-332; ASP-342; LYS-409; LYS-557; ARG-558; LYS-559;
RP   ARG-571; ARG-572 AND LYS-577.
RX   MEDLINE=21317458; PubMed=11423665;
RA   Oliver D., He D.Z.Z., Kloecker N., Ludwig J., Schulte U.,
RA   Waldegger S., Ruppersberg J.P., Dallos P., Fakler B.;
RT   "Intracellular anions as the voltage sensor of prestin, the outer hair
RT   cell motor protein.";
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RL   Science 292:2340-2343(2001).
CC   -!- FUNCTION: Motor protein that converts auditory stimuli to length
CC       changes in outer hair cells and mediates sound amplification in
CC       the mammalian hearing organ. Prestin is a bidirectional voltage-
CC       to-force converter, it can operate at microsecond rates. It uses
CC       cytoplasmic anions as extrinsic voltage sensors, probably chloride
CC       and bicarbonate. After binding to a site with millimolar affinity,
CC       these anions are translocated across the membrane in response to
CC       changes in the transmembrane voltage. They move towards the
CC       extracellular surface following hyperpolarization, and towards the
CC       cytoplasmic side in response to depolarization. As a consequence,
CC       this translocation triggers conformational changes in the protein
CC       that ultimately alter its surface area in the plane of the plasma
CC       membrane. The area decreases when the anion is near the
CC       cytoplasmic face of the membrane (short state), and increases when
CC       the ion has crossed the membrane to the outer surface (long
CC       state). So, it acts as an incomplete transporter. It swings anions
CC       across the membrane, but does not allow these anions to dissociate
CC       and escape to the extracellular space. Salicylate, an inhibitor of
CC       outer hair cell motility, acts as competitive antagonist at the
CC       prestin anion-binding site (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein; lateral wall of
CC       outer hair cells.
CC   -!- TISSUE SPECIFICITY: Specifically expressed in outer hair cells.
CC       Not detected in other cells of the organ of Corti.
CC   -!- DEVELOPMENTAL STAGE: Low levels are present in new-born rats and
CC       up to day 6. Subsequently, levels increase strongly. Adult levels
CC       are detected starting from day 9 in the basal turn of the cochlea,
CC       from day 10-11 in the middle turn, and from day 12 in the apical
CC       turn.
CC   -!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
CC       family.
CC   -!- SIMILARITY: Contains 1 STAS domain.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 22 of May 2002;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt022.html".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ303372; CAC21555.1; -.
DR   EMBL; AF315652; AAG30297.1; -.
DR   EMBL; AJ428404; CAD21439.1; -.
DR   InterPro; IPR002645; STAS.
DR   InterPro; IPR001902; Sulph_transpt.
DR   Pfam; PF01740; STAS; 1.
DR   Pfam; PF00916; Sulfate_transp; 1.
DR   TIGRFAMs; TIGR00815; sulP; 1.
DR   PROSITE; PS01130; SLC26A; 1.
DR   PROSITE; PS50801; STAS; 1.
KW   Motor protein; Cell shape; Transmembrane; Glycoprotein.
FT   DOMAIN        1     79       CYTOPLASMIC (POTENTIAL).
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FT   TRANSMEM     80    100       1 (POTENTIAL).
FT   DOMAIN      101    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    123       2 (POTENTIAL).
FT   DOMAIN      124    131       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    132    152       3 (POTENTIAL).
FT   DOMAIN      153    183       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    184    204       4 (POTENTIAL).
FT   DOMAIN      205    211       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    212    232       5 (POTENTIAL).
FT   DOMAIN      233    253       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    254    274       6 (POTENTIAL).
FT   DOMAIN      275    286       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    287    307       7 (POTENTIAL).
FT   DOMAIN      308    334       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    335    355       8 (POTENTIAL).
FT   DOMAIN      356    374       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    375    395       9 (POTENTIAL).
FT   DOMAIN      396    411       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    412    432       10 (POTENTIAL).
FT   DOMAIN      433    441       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    442    462       11 (POTENTIAL).
FT   DOMAIN      463    479       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    480    500       12 (POTENTIAL).
FT   DOMAIN      501    744       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      525    713       STAS.
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    166    166       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN     154    154       D->N: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE NEGATIVE VALUES.
FT   MUTAGEN     155    155       D->N: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE NEGATIVE VALUES.
FT   MUTAGEN     169    169       E->Q: NO EFFECT.
FT   MUTAGEN     177    177       K->Q: NO EFFECT.
FT   MUTAGEN     197    197       R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE NEGATIVE VALUES.
FT   MUTAGEN     233    233       K->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE NEGATIVE VALUES; WHEN ASSOCIATED
FT                                 WITH Q-235 AND Q-236.
FT   MUTAGEN     235    235       K->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE NEGATIVE VALUES; WHEN ASSOCIATED
FT                                 WITH Q-233 AND Q-236.
FT   MUTAGEN     236    236       R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE NEGATIVE VALUES; WHEN ASSOCIATED
FT                                 WITH Q-233 AND Q-235.
FT   MUTAGEN     277    277       E->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 SLIGHTLY MORE POSITIVE VALUES.
FT   MUTAGEN     281    281       R->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT                                 283 AND Q-285.
FT   MUTAGEN     283    283       K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT                                 218 AND Q-285.
FT   MUTAGEN     285    285       K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT                                 281-AND Q-283.
FT   MUTAGEN     332    332       D->Q: NO EFFECT.
FT   MUTAGEN     342    342       D->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                 MORE POSITIVE VALUES.
FT   MUTAGEN     409    409       K->Q: NO EFFECT.
FT   MUTAGEN     557    557       K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
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FT                                   558 AND Q-559.
FT   MUTAGEN      558    558         R->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT                                   557 AND Q-559.
FT   MUTAGEN      559    559         K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT                                   557 AND Q-558.
FT   MUTAGEN      571    571         R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                   SLIGHTLY MORE POSITIVE VALUES; WHEN
FT                                   ASSOCIATED WITH Q-572 AND Q-577.
FT   MUTAGEN      572    572         R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                   SLIGHTLY MORE POSITIVE VALUES; WHEN
FT                                   ASSOCIATED WITH Q-571 AND Q-577.
FT   MUTAGEN      577    577         K->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT                                   SLIGHTLY MORE POSITIVE VALUES; WHEN
FT                                   ASSOCIATED WITH Q-571 AND Q-572.
FT   CONFLICT     251    251         L -> V (IN REF. 2).
FT   CONFLICT     567    567         I -> M (IN REF. 2).
FT   CONFLICT     572    572         R -> S (IN REF. 2).
FT   CONFLICT     612    612         D -> G (IN REF. 2).
FT   CONFLICT     662    663         GI -> VM (IN REF. 2).
SQ   SEQUENCE   744 AA;  81278 MW;  E49E842CF7A3CD58 CRC64;

  Query Match             9.0%;  Score 84;  DB 1;  Length 744;
  Best Local Similarity   23.3%;  Pred. No. 11;
  Matches   61;  Conservative   34;  Mismatches   73;  Indels   94;  Gaps   12;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTV------------------FSIVSVTAYIALAL 44
              : | ::  :  ||:  | :|    |: |                  | :| | | ||:|:
Db        290 IPLEFFAVVMGTGISAGFNLHESYSVDVVGTLPLGLLPPANPDTSLFHLVYVDA-IAIAI 348

Qy         45 L--SVTISFR-----------------IYKGVIQAIQKSDEGHPFRAYLESEVAISEELV 85
              :  |||||                  |  |:  :|     |  |: :  |  ::|  ||
Db        349 VGFSVTISMAKTLANKHGYQVDGNQELIALGICNSI-----GSLFQTFSIS-CSLSRSLV 402

Qy         86 QKYSNSALGHVNC--TIKELRRLFLVDDLVDSLKFAVL---------------------- 121
              |: :        |  ::  |  :     | :||  |||
Db        403 QEGTGGKTQLAGCLASLMILLVILATGFLFESLPQAVLSAIVIVNLKGMFMQFSDLPFFW 462

Qy        122 --------MWVFTYVGALFNGL-----TLLILALISLFSVPVIYERHQAQIDHYLGLANK 168
                   :|: |:| :|| ||     | :|:||::     |||   : |   |  |
Db        463 RTSKIELTIWLTTFVSSLFLGLDYGLITAVIIALLT-----VIY---RTQSPSYTVLGQL 514

Qy        169 NVKDAMAKIQA-----KIPGLK 185
                 |    | |     :|||:|
Db        515 PDTDVYIDIDAYEEVKEIPGIK 536


RESULT 15
MDLB_BUCBP
ID   MDLB_BUCBP     STANDARD;      PRT;   578 AA.
AC   Q89A96;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Multidrug resistance-like ATP-binding protein mdlB.
GN   MDLB OR BBP424.
OS   Buchnera aphidicola (subsp. Baizongia pistaciae).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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OC   Enterobacteriaceae; Buchnera.
OX   NCBI_TaxID=135842;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426901; PubMed=12522265;
RA   Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA   Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA   Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT   "Reductive genome evolution in Buchnera aphidicola.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE014017; AAO27134.1; -.
DR   InterPro; IPR001140; ABC_TM_transpt.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   PROSITE; PS50929; ABC_TM1F; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Transport; Transmembrane; Complete proteome.
FT   TRANSMEM     26     46       POTENTIAL.
FT   TRANSMEM     59     79       POTENTIAL.
FT   TRANSMEM    143    163       POTENTIAL.
FT   TRANSMEM    166    186       POTENTIAL.
FT   TRANSMEM    196    216       POTENTIAL.
FT   TRANSMEM    260    280       POTENTIAL.
FT   DOMAIN      339    573       ABC TRANSPORTER.
FT   NP_BIND     373    380       ATP (POTENTIAL).
SQ   SEQUENCE   578 AA;  66827 MW;  3B84848CE196ADF7 CRC64;

  Query Match             8.9%;  Score 83;  DB 1;  Length 578;
  Best Local Similarity   20.3%;  Pred. No. 10;
  Matches   40;  Conservative   40;  Mismatches   63;  Indels   54;  Gaps    9;

Qy          1 SVVD-------LLYWRDIKKTGVVFGASLFLLLSL--------------------TV-FS 32
              :|:|       |||:    |  :: | :| |  |:                      || :|
Db          3 NVIDFWPTLKRLLYYGTNVKKYLILGFTLLLFSSIFEVLNPILISCFIKHYFINNTVNYS 62

Qy         33 IVSVTAYIALALLSVTISF-------RIYKGVIQA----IQKSDEGHPFRAYLESEVAIS 81
                :  :| |: | :|:  :::       :|   |||     :  |    | : : :  :
Db         63 LKIITYYLILQILAAILNYHQNIIFNKISLTVIQKLRYDVMSSTLQLPIKMFDQRPIG-- 120

Qy         82 EELVQKYSNSALGHVNCTIKEL-----RRLF--LVDDLVDSLKFAVLMWVFTYVGALFNG 134
               : : : :|        |||||     : ||  ::  |:  :   :| |    : ::
Db        121 -QFISRITNDTE-----TIKELYDTVIKSLFQNIILILITLITMFILEWRMACIASIIFP 174

Qy        135 LTLLILALISLFSVPVI 151
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                : |:|: |   || |::
Db        175 IALIIMLLYQYFSKPIL 191

Search completed: September 29, 2004, 18:14:47
Job time : 3.70944 secs
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